

SCORE Search Results Details for Application 10564585 and Search Result 20080623_150908_us-10-564-585-43.rng.

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This page gives you Search Results detail for the Application 10564585 and Search Result 20080623_150908_us-10-564-585-43.rng.

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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2008, 19:33:54 ; Search time 1326 Seconds
(without alignments)
22771.267 Million cell updates/sec

Title: US-10-564-585-43

Perfect score: 2797

Sequence: 1 ttcccccagcattcgagaaac.....aaaaaaaaaaaaaaaaggg 2797

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_200711:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000:*

4: geneseqn2001a:*

5: geneseqn2001b:*

6: geneseqn2002a:*

7: geneseqn2002b:*

8: geneseqn2003a:*

9: geneseqn2003b:*

10: geneseqn2003c:*

11: geneseqn2003d:*

12: geneseqn2004a:*

13: geneseqn2004b:*

14: geneseqn2004c:*

15: geneseqn2004d:*

16: geneseqn2005a:*

17: geneseqn2005b:*

18: geneseqn2005c:*

19: geneseqn2006a:*

20: geneseqn2006b:*

21: geneseqn2006c:*

22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2797	100.0	2797	6	ABL62724	Abi62724 Colon ade
2	2797	100.0	2797	6	ABV94033	Abv94033 Breast ca
3	2797	100.0	2797	8	ABX76311	Abx76311 Lung canc
4	2797	100.0	2797	8	ADB72273	Adb72273 Human SOX
5	2797	100.0	2797	9	ADA02535	Ada02535 Human SOX
6	2797	100.0	2797	10	ADH28813	Adh28813 Human chr
7	2797	100.0	2797	12	ACN38485	Acn38485 Tumour-as
8	2797	100.0	2797	16	ADW47984	Adw47984 Human sex
9	2797	100.0	2797	19	AEK60054	Aek60054 Human SOX
10	2797	100.0	2797	22	AEM95802	Aem95802 Human CML
11	2795.4	99.9	2797	9	ADE95783	Ade95783 Human DNA
12	2793	99.9	3233	8	ADB75556	Adb75556 Prostate
13	2765.8	98.9	4467	5	ABV22264	Abv22264 Human pro
14	2765.8	98.9	4467	5	ABV28101	Abv28101 Human pro
15	2765.8	98.9	4600	6	ABK39749	Abk39749 cDNA enco
16	2765.8	98.9	4600	8	ACA03264	Aca03264 Lung canc
17	2765.8	98.9	4600	8	ACA12078	Aca12078 Human lun
18	2765.8	98.9	4600	9	ADH47316	Adh47316 Human lun
19	2765.8	98.9	4600	12	ADJ21235	Adj21235 Human lun
20	2765.8	98.9	4600	19	AEH23893	Aeh23893 Human lun
21	2765.8	98.9	4912	16	ADX05998	Adx05998 Cyclin-de
22	2765.8	98.9	4912	16	ADZ80563	Adz80563 SRY (sex
23	2765.8	98.9	4912	16	AEA04382	Aea04382 Human cDN
24	2765.8	98.9	4912	16	AEH09647	Aeh09647 SRY (sex
25	2765.8	98.9	4912	19	AEJ48951	Aej48951 Human SRY
26	2765.8	98.9	22801	8	ADB72272	Adb72272 Human SOX
27	2765.8	98.9	22801	9	ADE95782	Ade95782 Human SOX
28	2765.8	98.9	22801	9	ADA02534	Ada02534 Human SOX
29	2765.8	98.9	22801	19	AEK60053	Aek60053 Human SOX
30	2761.2	98.7	4467	4	AHH72650	Aah72650 Human cer
31	2752.4	98.4	5892	9	ADF81488	Adf81488 Leukaemia
32	2752.4	98.4	5892	9	ADF81487	Adf81487 Leukaemia
33	2751.6	98.4	2802	7	AFS92546	Afs92546 Human tra
34	1807	64.6	8801	5	AAS45436	Aas45436 Chemicall
35	1807	64.6	8801	6	ABK28285	Abk28285 DNA trans
36	1807	64.6	8801	6	ABL33740	Abi133740 Human imm
c 37	1721.6	61.6	8801	5	AAS45437	Aas45437 Chemicall
c 38	1721.6	61.6	8801	6	ABK28286	Abk28286 DNA trans
c 39	1721.6	61.6	8801	6	ABL33741	Abi133741 Human imm
40	1425	50.9	1425	8	ADB72274	Adb72274 Human SOX
41	1425	50.9	1425	9	ADE95784	Ade95784 Human SOX
42	1425	50.9	1425	9	ADA02536	Ada02536 Human SOX
43	1425	50.9	1425	12	ACH87117	Ach87117 Human gen
44	1425	50.9	1425	19	AEK60055	Aek60055 Human SOX
c 45	1016	36.3	1584	6	ABQ32052	Abq32052 Oligonucl

ALIGNMENTS

RESULT 1
 ABL62724
 ID ABL62724 standard; DNA; 2797 BP.
 XX
 AC ABL62724;
 XX
 DT 11-JUN-2007 (revised)

DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1061.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
DR PC:NCBI; gi36552.

DR PC_ENCPRO:NCBI; gi36553.

XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

XX

PS Claim 1; SEQ ID NO 1061; 44pp; English.

XX

CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 6; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCCCAGCATTGAGAAAATCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60

Db 1 TTCCCCAGCATTGAGAAAATCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60

Qy 61 ACAGCAAATCGCAGCGGGTGAGAGAGGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120

Db 61 ACAGCAAATCGCAGCGGGTGAGAGAGGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120

Qy 121 GGAACATAACTCCTCTCGAGAGCGGAGAACTCCTCCCCAATCTTTGGGACTTT 180

Db 121 GGAACATAACTCCTCTCGAGAGCGGAGAACTCCTCCCCAATCTTTGGGACTTT 180

Qy 181 TCTCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGGCAGTTCGGCCGCCGCG 240

Db 181 TCTCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGGCAGTTCGGCCGCCGCG 240

Qy 241 CGTCTTCCCGTTCGGCGTGTGCTTGGCCCGGGGAAACGGGGAGGGCCGGATCGCGGG 300

Db 241 CGTCTTCCCGTTCGGCGTGTGCTTGGCCCGGGGAAACGGGGAGGGCCGGATCGCGGG 300

Qy 301 CGGCCGCCGCGAGGGTGAGCGCGCGTGGGCCGCCGCCGAGCCGAGGGCATGGTGAGC 360

Db 301 CGGCCGCCGCGAGGGTGAGCGCGCGTGGGCCGCCGCCGAGCCGAGGGCATGGTGAGC 360

Qy 361 AAACCAACAAATGCCAGAACCGGAAGCGCTGCTGGCCGCCAGAGCTCGGACTCGGGC 420

Db 361 AAACCAACAAATGCCAGAACCGGAAGCGCTGCTGGCCGCCAGAGCTCGGACTCGGGC 420

Qy 421 CGGGCCTCGAGCTGGGAATCGCCTCCCTCCACGCCGGCTCCACCGCCTCACGGCG 480

Db 421 CGGGCCTCGAGCTGGGAATCGCCTCCCTCCACGCCGGCTCCACCGCCTCACGGCG 480

Qy	481	GCAAGGCCGACGCCCGAGCTGGTCAAGACCCGAGTGGCACATCAAGGCCCATGA	540
Db	481		540
Qy	541	ACGCCCTCATGGTGCTGGCAGATCGAGCGGCAGAAGTCATGGAGCAGTCGCCGACA	600
Db	541		600
Qy	601	TGCACAACGCCGAGATCTCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG	660
Db	601		660
Qy	661	ACAAGATCCCTTCATTGAGAGCGGGAGCGCTGCGCTCAAGCACATGGCTGACTACC	720
Db	661		720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACCCAACCTCAGCTCT	780
Db	721		780
Qy	781	CGGCCGCCCTCCCAAGCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGGGGG	840
Db	781		840
Qy	841	CGGGCATGGGGCGGGCGGGCGGGCGGGAGCAGCAACCGGGGGAGGAGGCGGGT	900
Db	841		900
Qy	901	CGAGTGGCGGGCGGCCAACCTCAAACCGGCCAGAAAAGAGCTGCGCTCAAAGTGG	960
Db	901		960
Qy	961	CGGGCGGCCGGGGGGTAGCAAAACCGCACGCCAACGCTCATCTGGCAGGCCG	1020
Db	961		1020
Qy	1021	CGGGCGGGGGAAAGCACGCCCTGCCGCCCTCTGCCGCCAACAGGGGGGG	1080
Db	1021		1080
Qy	1081	CGGCCGCCCTGCTGCCCTGGGCCGCCGCCGACCACTCGCTGTACAAGGCCGGA	1140
Db	1081		1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCGGCCAGCCTCGGCCAGCGCTCGGCC	1200
Db	1141		1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTACCTGTTGGGGCTGGCA	1260
Db	1201		1260
Qy	1261	CGTCGTCGCCGTGGCGCGCTGGCGCGGGAGCGACCCAGCGACCCCCCTGGCC	1320
Db	1261		1320
Qy	1321	TGTAGCAGGAGGAGGGCCGGCTGCTGCCAGCGCCCGAGCTGAGGCCGCCAGCA	1380
Db	1321		1380
Qy	1381	GCGCCGCCCTGCCCCGCCGCCGCTGCCCGGCCGACCCCGCGCTACGCCAGCC	1440
Db	1381		1440
Qy	1441	TGCGGCCGCCCTGCCCGCCCGTCCAGCGGCCCTCGCACCGCTCTCCCTGGCTCG	1500
Db	1441		1500

Qy	1501	CCCACTCCTCCTTCCTCCTCGGGCTCCTCGCTCCGACGACGAGTCGAAGACG 1560
Db	1501	CCCACTCCTCCTTCCTCCTCGGGCTCCTCGCTCCGACGACGAGTCGAAGACG 1560
Qy	1561	ACCTGCTCGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGGAGCTTCAGTT 1620
Db	1561	ACCTGCTCGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGGAGCTTCAGTT 1620
Qy	1621	CGTCGTCGGCCTGCACGGGACCTGGATTAACTCGAGCCCCGGCTCCGGCTCGCACT 1680
Db	1621	CGTCGTCGGCCTGCACGGGACCTGGATTAACTCGAGCCCCGGCTCCGGCTCGCACT 1680
Qy	1681	TCGAGTTCCCGGACTACTGACGCCGGGGTGAAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Db	1681	TCGAGTTCCCGGACTACTGACGCCGGGGTGAAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Qy	1741	AGTCAGCATTCACCTGGTTTACCTACTGAAGGGCGCGAGCAGGGAGAAGGGC 1800
Db	1741	AGTCAGCATTCACCTGGTTTACCTACTGAAGGGCGCGAGCAGGGAGAAGGGC 1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGAACGAAAAGACAGCAA 1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGAACGAAAAGACAGCAA 1860
Qy	1861	GAGTTAAAGGAGAAAGGGAAAAAGAACGAAAAGTAAAGCAGGGCTCGTTCGCCCCGCT 1920
Db	1861	GAGTTAAAGGAGAAAGGGAAAAAGAACGAAAAGTAAAGCAGGGCTCGTTCGCCCCGCT 1920
Qy	1921	TCTCGTCGGATCAAGGAGCGCGGGCGTTTGACCGCGCTCCCATCCCCACCT 1980
Db	1921	TCTCGTCGGATCAAGGAGCGCGGGCGTTTGACCGCGCTCCCATCCCCACCT 1980
Qy	1981	TCCCGGGCGGGGACCCACTCTGCCACGCCGGAGGGACGCCGGAGGAGGAAGGGTAGAC 2040
Db	1981	TCCCGGGCGGGGACCCACTCTGCCACGCCGGAGGGACGCCGGAGGAGGAAGGGTAGAC 2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGCGAC 2100
Db	2041	AGGGCGACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGCGAC 2100
Qy	2101	TTCGAGTTGCTCCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC 2160
Db	2101	TTCGAGTTGCTCCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC 2160
Qy	2161	TTGCTGCACCCCCAGAACAGGGCAGTTAGTTCTAGAGACTGAAGGAGCTCCCC 2220
Db	2161	TTGCTGCACCCCCAGAACAGGGCAGTTAGTTCTAGAGACTGAAGGAGCTCCCC 2220
Qy	2221	CTTCTGCATACCACCTGGTTTGTGTTTAAACCGGTGATGAAGACAGAAGGCTCCGG 2280
Db	2221	CTTCTGCATACCACCTGGTTTGTGTTTAAACCGGTGATGAAGACAGAAGGCTCCGG 2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGGTGATGAAGACAGAAGGCTCCGG 2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGGTGATGAAGACAGAAGGCTCCGG 2340
Qy	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Db	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Qy	2401	GCAGGCGAATTCCTGGGGCTTTTCTCCCTCTTCCCTGGCCCTCTGC 2460
Db	2401	GCAGGCGAATTCCTGGGGCTTTTCTCCCTCTTCCCTGGCCCTCTGC 2460
Qy	2461	AGCGGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCTGTAACGGGGCTAGGAAATG 2520

Db	2461 AGCGGAGGAGGAGATGGTGGAGGGAGGCCAGCCAGTGACCGCGCTAGGAATG	2520
Qy	2521 ACCCGAGAACCCCGTTGAGCGCAGCAGCGGAGCTAGGGCGGGGGCGAGGAGACA	2580
Db	2521 ACCCGAGAACCCCGTTGAGCGCAGCAGCGGAGCTAGGGCGGGGGCGAGGAGACA	2580
Qy	2581 CGAACTGGAACGGGTTCACGGTCAAACGTAAATGGATTGCACGTTGGGAGCTGGCG	2640
Db	2581 CGAACTGGAACGGGTTCACGGTCAAACGTAAATGGATTGCACGTTGGGAGCTGGCG	2640
Qy	2641 CGGCGGCTGCTGGGCCTCCGCCTCTTCTACGTGAAATCAGTGAGGTGAGACTTCCC	2700
Db	2641 CGGCGGCTGCTGGGCCTCCGCCTCTTCTACGTGAAATCAGTGAGGTGAGACTTCCC	2700
Qy	2701 GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGTCAGGGCAGTCAGTGGAG	2760
Db	2701 GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGTCAGGGCAGTCAGTGGAG	2760
Qy	2761 GGCGAGTGGTTTCGAAAAAAAAAAAAAGAAAAAAAGGG	2797
Db	2761 GGCGAGTGGTTTCGAAAAAAAAAAAAAGAAAAAAAGGG	2797

RESULT 2

ABV94033

ID ABV94033 standard; cDNA; 2797 BP.

XX

AC ABV94033;

XX

DT 11-JUN-2007 (revised)

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:24.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB002811.

XX

PR 08-DEC-2000; 2000US-0254090P.

PR 07-DEC-2001; 2001US-00007926.

XX

PA (IPSO-) IPSOGEN.

XX

PI Bertucci F, Houlgate R, Birnbaum D, Nguyen C, Viens P, Fert V;

XX

DR WPI; 2002-619023/66.

DR PC:NCBI; gi36552.

DR PC_ENCPRO:NCBI; gi36553.

XX

PT Novel polynucleotide library useful in molecular characterization of a carcinoma, comprising a pool of polynucleotide sequences or its subsequences which are either underexpressed or overexpressed in tumor cells.

XX

PS Claim 1; Page 124-125; 40lpp; English.

XX

CC The present invention describes a polynucleotide library (I) useful in CC the molecular characterisation of a carcinoma, comprising a pool of CC polynucleotides or its subsequences which are either underexpressed or CC overexpressed in tumour cells, and correspond to any of the

CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
 CC (M1) differentially expressed polynucleotide sequences which are
 CC correlated with a cancer, involves obtaining a polynucleotide sample from
 CC a patient, and reacting the polynucleotide sample obtained with a probe
 CC immobilised on a solid support, where the probe comprises any combination
 CC of the polynucleotide sequences of (I) or its expression products encoded
 CC by polynucleotide sequences of (I), and detecting the reaction product.
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
 CC useful for the prognosis or diagnostic of tumour, in differentiating a
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour
 CC cell, differentiating a tumour with lymph nodes from a tumour without
 CC lymph nodes, differentiating antracycline-sensitive tumours from
 CC antracycline-insensitive tumours, and classifying good and poor prognosis
 CC primary breast tumours. (I) is useful for large-scale molecular
 CC characterisation of breast cancer that help in prediction, prognosis and
 CC cancer treatment, and for detecting differentially expressed genes that
 CC correlated with a cancer
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 6; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTCCCCAGCATTCGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Db	1	TTCCCCAGCATTCGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Qy	61	ACAGCAAACCTGCAGCGCGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120
Db	61	ACAGCAAACCTGCAGCGCGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120
Qy	121	GGAACTATAACTCCTCTCGAGAGGGCGAGAACTCCTCCCCAATCTTTGGGACTTT 180
Db	121	GGAACTATAACTCCTCTCGAGAGGGCGAGAACTCCTCCCCAATCTTTGGGACTTT 180
Qy	181	TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGCCAGTTCGGGCGCGCGCG 240
Db	181	TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGCCAGTTCGGGCGCGCGCG 240
Qy	241	CGTCTCCCGTTCGGCGTGTCTTGGCCGGGGAACCGGGAGGGCCCGCGATCCCGGG 300
Db	241	CGTCTCCCGTTCGGCGTGTCTTGGCCGGGGAACCGGGAGGGCCCGCGATCCCGGG 300
Qy	301	CGGCCGCCGCGAGGGTGTAGCGCGCTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360
Db	301	CGGCCGCCGCGAGGGTGTAGCGCGCTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360
Qy	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGAGAGCTGGACTCGGGC 420
Db	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGAGAGCTGGACTCGGGC 420
Qy	421	CCGGCCTCGAGCTGGGAATGCCCTCCCTCCACGCCGGCTCCACCGCCCTCACGGGC 480
Db	421	CCGGCCTCGAGCTGGGAATGCCCTCCCTCCACGCCGGCTCCACCGCCCTCACGGGC 480
Qy	481	GCAAGGGCGACGACCCGAGCTGGTGCAGAACCCCCGAGTGGGCACATCAAGGGACCCATGA 540
Db	481	GCAAGGGCGACGACCCGAGCTGGTGCAGAACCCCCGAGTGGGCACATCAAGGGACCCATGA 540
Qy	541	ACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCGACA 600

Db	541	ACGCCTTCATGGTGTGGCGCAGATCAGGCCGCAAGATCATGGAGCAGTCGCCGACA	600
Qy	601	TGACAACGCCAGATCTCAAAGCCGCTGGCCAACCGCTGGAAGCTGCTCAAAAGACAGG	660
Db	601	TGACAACGCCAGATCTCAAAGCCGCTGGCCAACCGCTGGAAGCTGCTCAAAAGACAGG	660
Qy	661	ACAAGATCCCTTCATTGAGAGCCGAGCCGCTGCGCTCAAGCACATGGTACTACC	720
Db	661	ACAAGATCCCTTCATTGAGAGCCGAGCCGCTGCGCTCAAGCACATGGTACTACC	720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACCTCAGCTCT	780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACCTCAGCTCT	780
Qy	781	CGGCCGCGCCCTCTCCAAGCCGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGG	840
Db	781	CGGCCGCGCCCTCTCCAAGCCGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGG	840
Qy	841	GCGGCCATGGGGCGCGCCGGCGCGCGGGAGACAGCAGCAACCGGGGGAGGAGCCGGGTG	900
Db	841	GCGGCCATGGGGCGCGCCGGCGCGGGAGACAGCAGCAACCGGGGGAGGAGCCGGGTG	900
Qy	901	CGAGTGGCCGGGGGCCAACCTCAAACCGGGCGAGAAAAAGAGCTGCGCTCAAAGTGG	960
Db	901	CGAGTGGCCGGGGGCCAACCTCAAACCGGGCGAGAAAAAGAGCTGCGCTCAAAGTGG	960
Qy	961	CGGGCGGCGGGGGCGGTGGGTTAGCAAACCGCACGCCAACGCTCATCTGGCAGGGCG	1020
Db	961	CGGGCGGCGGGGGCGGTGGGTTAGCAAACCGCACGCCAACGCTCATCTGGCAGGGCG	1020
Qy	1021	GCGGCCGGGGAAAGCAGCGCTGCCGCCGCCGCCCTCTCGCCGCCAACAGCGGGGG	1080
Db	1021	GCGGCCGGGGAAAGCAGCGCTGCCGCCGCCCTCTCGCCGCCAACAGCGGGGG	1080
Qy	1081	CCGCGGCCCTGCTGCCCTGGGCCGCCGCCGCCGACCCACTCGCTGTACAAGGCGCGGA	1140
Db	1081	CCGCGGCCCTGCTGCCCTGGGCCGCCGCCGCCGACCCACTCGCTGTACAAGGCGCGGA	1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCTCGGAGCCTCGGCCCTCCGACCGCTGGGCC	1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCTCGGAGCCTCGGCCCTCCGACCGCTGGGCC	1200
Qy	1201	CGGCAAGCACCTGGCGAGAAGAAGGTGAAGCAGCGCTACCTGTCGGCGCCCTGGCA	1260
Db	1201	CGGCAAGCACCTGGCGAGAAGAAGGTGAAGCAGCGCTACCTGTCGGCGCCCTGGCA	1260
Qy	1261	CGTCGTCGTGCCCGTGGCGCGTGGCGCGGGAGCCGACCCAGCGACCCCTGGCC	1320
Db	1261	CGTCGTCGTGCCCGTGGCGCGTGGCGCGGGAGCCGACCCAGCGACCCCTGGCC	1320
Qy	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCCGACGCCAGCGCCGAGCGCACAGCA	1380
Db	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCCGACGCCAGCGCCGAGCGCACAGCA	1380
Qy	1381	GCGGCCCTCGTCCCCCGCCGCCGCCCTGCCGCCGCCACCCAGCGCTACGCCAGC	1440
Db	1381	GCGGCCCTCGTCCCCCGCCGCCGCCCTGCCGCCGCCACCCAGCGCTACGCCAGC	1440
Qy	1441	TGCCCGCCGCCCTGCCCGCCCGTCCAGCGCCCTCCAGCGCTCTCTCGGCCCTG	1500
Db	1441	TGCCCGCCGCCCTGCCCGCCCGTCCAGCGCCCTCCAGCGCTCTCTCGGCCCTG	1500
Qy	1501	CCCACTCCCTCTCCCTCCCTCCCTCCGGCTCTCGCTCTCCAGCGAGCTCGAAGACG	1560
Db	1501	CCCACTCCCTCTCCCTCCCTCCGGCTCTCGCTCTCCAGCGAGCTCGAAGACG	1560

Qy	1561	ACCTGCTGCACCTGAACCCAGCTCAAATTGGAGAGCATGCCCTGGCAGCTTCAGTT 	1620
Db	1561	ACCTGCTGCACCTGAACCCAGCTCAAATTGGAGAGCATGCCCTGGCAGCTTCAGTT 	1620
Qy	1621	CGTCGTCGGCCTGCACCGGACCTGGATTAACTTCGAGCCCCGCTCCGGCTCGCACT 	1680
Db	1621	CGTCGTCGGCCTGCACCGGACCTGGATTAACTTCGAGCCCCGCTCCGGCTCGCACT 	1680
Qy	1681	TCGAGTTCCCGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 	1740
Db	1681	TCGAGTTCCCGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 	1740
Qy	1741	AGTCAGCATCTCCAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC 	1800
Db	1741	AGTCAGCATCTCCAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC 	1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA 	1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA 	1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAGAACGAGCTCGTTCGCCCGCT 	1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAGAACGAGCTCGTTCGCCCGCT 	1920
Qy	1921	TCTCGTCGGATCAAGGAGCGCGCGCGTTGGACCCGCGTCCCATCCCCACCT 	1980
Db	1921	TCTCGTCGGATCAAGGAGCGCGCGCGTTGGACCCGCGTCCCATCCCCACCT 	1980
Qy	1981	TCCGGGGCGGGGACCACACTGCCCACGCCGGAGGGACGCCGGAGGGAGAGGTAGAC 	2040
Db	1981	TCCGGGGCGGGGACCACACTGCCCACGCCGGAGGGACGCCGGAGGGAGAGGTAGAC 	2040
Qy	2041	AGGGGCACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGCGAC 	2100
Db	2041	AGGGGCACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGCGAC 	2100
Qy	2101	TTCGAGTTGCTCCCTTGTGTTGAAGAGACCCCTCCCTTCCAACGAGCTTCCGGAC 	2160
Db	2101	TTCGAGTTGCTCCCTTGTGTTGAAGAGACCCCTCCCTTCCAACGAGCTTCCGGAC 	2160
Qy	2161	TTGTCGACCCCCAGCAAGAGCGAGTTAGTTCTAGAGACTGAAGGAGCTCCCC 	2220
Db	2161	TTGTCGACCCCCAGCAAGAGCGAGTTAGTTCTAGAGACTGAAGGAGCTCCCC 	2220
Qy	2221	CTTCCTGCATCACCACTTGGTTTATTTGCTCTTGGTCAGAAAGGAGGGGA 	2280
Db	2221	CTTCCTGCATCACCACTTGGTTTATTTGCTCTTGGTCAGAAAGGAGGGGA 	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACGCGTGTGAAGACAGAAGGCTCCGG 	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACGCGTGTGAAGACAGAAGGCTCCGG 	2340
Qy	2341	GGTGACGAATTGGCCGATGCCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC 	2400
Db	2341	GGTGACGAATTGGCCGATGCCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC 	2400
Qy	2401	GCAGCGAATTCCCGTTGGGGCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 	2460
Db	2401	GCAGCGAATTCCCGTTGGGGCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 	2460
Qy	2461	AGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAATG 	2520
Db	2461	AGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAATG 	2520
Qy	2521	ACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGCGGGGGCGAGGAGGACA 	2580
Db	2521	ACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGCGGGGGCGAGGAGGACA 	2580

Qy 2581 CGAACTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGCACGTTGGGGAGCTGGCGG 2640
 |||||||
 Db 2581 CGAACTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGCACGTTGGGGAGCTGGCGG 2640
 Qy 2641 CGGCGGCTGCTGGGCCCTCCGCCTTCTTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
 |||||||
 Db 2641 CGGCGGCTGCTGGGCCCTCCGCCTTCTTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
 Qy 2701 GACCCCGGAGGCCTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG 2760
 |||||||
 Db 2701 GACCCCGGAGGCCTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG 2760
 Qy 2761 GGCGAGTGGTTCCGAAAAAAAAGAAAAAGGG 2797
 |||||||
 Db 2761 GGCGAGTGGTTCCGAAAAAAAAGAAAAAGGG 2797

RESULT 3

ABX76311

ID ABX76311 standard; DNA; 2797 BP.

XX

AC ABX76311;

XX

DT 11-JUN-2007 (revised)

DT 02-APR-2003 (first entry)

XX

DE Lung cancer-associated polynucleotide #175.

XX

KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX

OS Unidentified.

XX

PN WO200286443-A2.

XX

PD 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US012476.

XX

PR 18-APR-2001; 2001US-0284770P.

PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Aziz N, Murray R;

XX

DR WPI; 2003-093161/08.

DR P-PSDB; ABU56582.

DR PC:NCBI; gi36552.

XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.

XX

PS Claim 22; Page 322-323; 453pp; English.

XX

CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological

CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 8; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 TTCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Db	1 TTCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Qy	61 ACAGCAAACGTGAGCGCGGTGAGAGAGCGAGAGAGAGAGAGAGACTCTCCAGCCTG 120
Db	61 ACAGCAAACGTGAGCGCGGTGAGAGAGCGAGAGAGAGAGAGAGACTCTCCAGCCTG 120
Qy	121 GGAACATAACTCCTCTGCAGAGGGCGAGAACTCCTTCCCCAATCTTTGGGACTTT 180
Db	121 GGAACATAACTCCTCTGCAGAGGGCGAGAACTCCTTCCCCAATCTTTGGGACTTT 180
Qy	181 TCTCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGCCAGTTGGCCGCGCG 240
Db	181 TCTCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGCCAGTTGGCCGCGCG 240
Qy	241 CGTCTCCCGTTCGCGTGTGCTTGGCCGGGAACCGGGAGGGCCGGATCGCGCG 300
Db	241 CGTCTCCCGTTCGCGTGTGCTTGGCCGGGAACCGGGAGGGCCGGATCGCGCG 300
Qy	301 CGGCCGCCGCGAGGGTGTGAGCGCGTGGCGCCGGAGCCGAGGCCATGGTCAGC 360
Db	301 CGGCCGCCGCGAGGGTGTGAGCGCGTGGCGCCGGAGCCGAGGCCATGGTCAGC 360
Qy	361 AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCGCGAGAGCTGGACTCGGGCG 420
Db	361 AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCGCGAGAGCTGGACTCGGGCG 420
Qy	421 CGGCCCTCGAGCTGGGAATCGCTCTCCCCACGCCCGGCTCCACCGCCCTCCACGGCG 480
Db	421 CGGCCCTCGAGCTGGGAATCGCTCTCCCCACGCCCGGCTCCACCGCCCTCCACGGCG 480
Qy	481 GCAAGGGCGACGACCCCAGCTGGTCAAGACCCCCGAGTGGCACATCAAGGGACCCATGA 540
Db	481 GCAAGGGCGACGACCCCAGCTGGTCAAGACCCCCGAGTGGCACATCAAGGGACCCATGA 540
Qy	541 ACGCCCTCATGGTGTGCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCGACA 600
Db	541 ACGCCCTCATGGTGTGCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCGACA 600

Qy	601	TGCACAAACGCCAGATCTCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Db	601	TGCACAAACGCCAGATCTCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Qy	661	ACAAGATCCCTTCATTGAGAGGGAGCAGCGCTGCCTCAAGCACATGGCTGACTACC 720
Db	661	ACAAGATCCCTTCATTGAGAGGGAGCAGCGCTGCCTCAAGCACATGGCTGACTACC 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Qy	781	CGGCCGCCGCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGTCGGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCGCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGTCGGTGGCAGTGGCGGG 840
Qy	841	GCGGCATGGGGCGCGGGCGCGGGAGCAGCAACGCCGGGGAGGAGGCCGGCTG 900
Db	841	GCGGCATGGGGCGCGGGCGCGGGAGCAGCAACGCCGGGGAGGAGGCCGGCTG 900
Qy	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCAAAGTGG 960
Db	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCAAAGTGG 960
Qy	961	CGGGCGGCAGGGGGTAGAACCGCACGCCAACGCTCATCCTGGCAGGCCGG 1020
Db	961	CGGGCGGCAGGGGGTAGAACCGCACGCCAACGCTCATCCTGGCAGGCCGG 1020
Qy	1021	GCGGGCGGGAAAGCACGCCGTGCCGCCGCCCTCTGGCGAGGCCAGGGGGGG 1080
Db	1021	GCGGGCGGGAAAGCACGCCGTGCCGCCGCCCTCTGGCGAGGCCAGGGGGGG 1080
Qy	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Db	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCTGGCAGGCCCTCCGCCAGCGCTCGGGCCC 1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCTGGCAGGCCCTCCGCCAGCGCTCGGGCCC 1200
Qy	1201	CGGGCAAGCACCTGGCGGAGAAGGTGAAGCGCGTCACTGTTGCCGCCCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGGAGAAGGTGAAGCGCGTCACTGTTGCCGCCCTGGCA 1260
Qy	1261	CGTCGTCGCGCCCTGGCGGGCTGGCGCGGGAGCCGACCCCCAGCGACCCCCCTGGGCC 1320
Db	1261	CGTCGTCGCGCCCTGGCGGGCTGGCGCGGGAGCCGACCCCCAGCGACCCCCCTGGGCC 1320
Qy	1321	TGTACGAGGAGGAGGGCGGGCTGCTGCCAGCGGCCAGCCTGAGCGGCCAGCA 1380
Db	1321	TGTACGAGGAGGAGGGCGGGCTGCTGCCAGCGGCCAGCCTGAGCGGCCAGCA 1380
Qy	1381	GCGCCGCCTCGCCCCCGCCGCCCTGCCGCCGACCACCGCGCTACGCCAGCC 1440
Db	1381	GCGCCGCCTCGCCCCCGCCGCCCTGCCGCCGACCACCGCGCTACGCCAGCC 1440
Qy	1441	TGCGCGCCGCCCTGCCCTCCGCCAGCGGCCCTGCCAGCGCTCTCTGGCTCGT 1500
Db	1441	TGCGCGCCGCCCTGCCCTCCGCCAGCGGCCCTGCCAGCGCTCTCTGGCTCGT 1500
Qy	1501	CCCACTCCCTCTTCTCTCTCGGCCAGCTGACGAGCTTCGAAGACG 1560
Db	1501	CCCACTCCCTCTTCTCTCTCGGCCAGCTGACGAGCTTCGAAGACG 1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAACCTTGAGAGCATGTCCTGGCAGCTCAGTT 1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAACCTTGAGAGCATGTCCTGGCAGCTCAGTT 1620

Qy	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTTCGAGCCCCGCTCCGGCTCGCACT	1680
Db	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTTCGAGCCCCGCTCCGGCTCGCACT	1680
Qy	1681	TCGAGTTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTG	1740
Db	1681	TCGAGTTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTG	1740
Qy	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC	1800
Db	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC	1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGRAACGAAAGGACAGACGAA	1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAGAAAAGRAACGAAAGGACAGACGAA	1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAAAAGAAAAAGTAAGCAGGGCTCGTCGCCCGCT	1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAAAAGAAAAAGTAAGCAGGGCTCGTCGCCCGCT	1920
Qy	1921	TCTCGTCGGATCAAGGAGCGCGCGCGTTGGACCCGCGCTCCCATCCCCACCT	1980
Db	1921	TCTCGTCGGATCAAGGAGCGCGCGCGTTGGACCCGCGCTCCCATCCCCACCT	1980
Qy	1981	TCCCGGGCGGGGACCACACTGCCAGCCGAGGGACCGGGAGGAGAAGAGGGTAGAC	2040
Db	1981	TCCCGGGCGGGGACCACACTGCCAGCCGAGGGACCGGGAGGAGAAGAGGGTAGAC	2040
Qy	2041	AGGGCGCACCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAAAGCGAC	2100
Db	2041	AGGGCGCACCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAAAGCGAC	2100
Qy	2101	TTCGAGTTGTCCTTGTGAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Db	2101	TTCGAGTTGTCCTTGTGAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Qy	2161	TTGTCGCACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTTGAAGGAGTCTCCC	2220
Db	2161	TTGTCGCACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTTGAAGGAGTCTCCC	2220
Qy	2221	CTTCCTGCATCACCACTTGGTTTGTATTGCTTGTGTCAGAAAGGAGGGAA	2280
Db	2221	CTTCCTGCATCACCACTTGGTTTGTATTGCTTGTGTCAGAAAGGAGGGAA	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAAGGCTCGG	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAAGGCTCGG	2340
Qy	2341	GGTGACGAATTGGCCGATGCCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Db	2341	GGTGACGAATTGGCCGATGCCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Qy	2401	GCAGCGAATTCCCGTTGGGGCTTTTCTCCCTTCCCTGGCCCTCTGC	2460
Db	2401	GCAGCGAATTCCCGTTGGGGCTTTTCTCCCTTCCCTGGCCCTCTGC	2460
Qy	2461	AGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Db	2461	AGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGCGGGGGAGGAGGACA	2580
Db	2521	ACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGCGGGGGAGGAGGACA	2580
Qy	2581	CGAACCTGAAAGGGGTTCACCGTAAACTGAATGGATTGCACTGGAGCTGGCGG	2640

Db	2581 CGAACTGGAAGGGGTTCACGGTCAAACGTGAAATGGATTGACGGTGGGAGCTGGCGG 2640
Qy	2641 CGGGCGCTGCTGGGCCTCCGCCTCTTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
Db	2641 CGGGCGCTGCTGGGCCTCCGCCTCTTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
Qy	2701 GACCCCGGAGGCCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGGCAGTCAGTGGAG 2760
Db	2701 GACCCCGGAGGCCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGGCAGTCAGTGGAG 2760
Qy	2761 GGCGAGTGGTTCGGAAAAAAAAAGAAAAAAAGGG 2797
Db	2761 GGCGAGTGGTTCGGAAAAAAAAAGAAAAAAAGGG 2797

RESULT 4

ADB72273

ID ADB72273 standard; mRNA; 2797 BP.

XX

AC ADB72273;

XX

DT 11-JUN-2007 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Human SOX4 mRNA.

XX

KW human; ss; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;

KW cancer; neoplasm; adenocarcinoma; sarcoma.

XX

OS Homo sapiens.

XX

PN WO2003008583-A2.

XX

PD 30-JAN-2003.

XX

PF 26-DEC-2001; 2001WO-US051291.

XX

PR 02-MAR-2001; 2001US-00798586.

PR 23-OCT-2001; 2001US-00004113.

PR 08-NOV-2001; 2001US-00052482.

PR 30-NOV-2001; 2001US-00997722.

PR 20-DEC-2001; 2001US-00034650.

XX

PA (SAGR-) SAGRES DISCOVERY.

XX

PI Morris DW, Engelhard EK;

XX

DR WPI; 2003-239337/23.

DR PC:NCBI; gi36552.

DR PC_ENCPRO:NCBI; gi36553.

XX

PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.

XX

PS Claim 1; SEQ ID NO 101; 2304pp; English.

XX

CC The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human mRNA of the invention.

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.

CC

SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 8; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
 |||||||

Db 1 TTCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60

Qy 61 ACAGCAAATCGAGCGCGTAGAGAGCGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120
 |||||||

Db 61 ACAGCAAATCGAGCGCGTAGAGAGCGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120

Qy 121 GGAACATAACTCCTCTCGAGAGCGGAGAACCTCTCCCCAATCTTTGGGACTTT 180
 |||||||

Db 121 GGAACATAACTCCTCTCGAGAGCGGAGAACCTCTCCCCAATCTTTGGGACTTT 180

Qy 181 TCTCTTTACCCACCTCCGCCCTCGAGAGGAGTTGAGGGGCAGTTCGGCCGCGCG 240
 |||||||

Db 181 TCTCTTTACCCACCTCCGCCCTCGAGAGGAGTTGAGGGGCAGTTCGGCCGCGCG 240

Qy 241 CGTCTCCCGTTCGGCGTGTCTTGGCCGGAAACCGGGAGGGCCGATCGCGCG 300
 |||||||

Db 241 CGTCTCCCGTTCGGCGTGTCTTGGCCGGAAACCGGGAGGGCCGATCGCGCG 300

Qy 301 CGGCCGCGCGAGGGTGAGCGCGCTGGGCCCGCCGAGCCGAGGCCATGGTGCGAC 360
 |||||||

Db 301 CGGCCGCGCGAGGGTGAGCGCGCTGGGCCCGCCGAGCCGAGGCCATGGTGCGAC 360

Qy 361 AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCCGGAGAGCTCGACTGGCG 420
 |||||||

Db 361 AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCCGGAGAGCTCGACTGGCG 420

Qy 421 CGGCCCTCGAGCTGGAAATCGCTCTCCCCACGCCGGCTCACGCCCTCACGGCG 480
 |||||||

Db 421 CGGCCCTCGAGCTGGAAATCGCTCTCCCCACGCCGGCTCACGCCCTCACGGCG 480

Qy 481 GCAAGGCCGACGCCAGCTGGTCAAGACCCCCGAGTGGGCACATCAAGGCCCATGA 540
 |||||||

Db 481 GCAAGGCCGACGCCAGCTGGTCAAGACCCCCGAGTGGGCACATCAAGGCCCATGA 540

Qy 541 ACGCTTCATGGTGTGGTCAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCGACA 600
 |||||||

Db 541 ACGCTTCATGGTGTGGTCAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCGACA 600

Qy 601 TGCACAACGCCAGATCTCAAGCGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGG 660
 |||||||

Db 601 TGCACAACGCCAGATCTCAAGCGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGG 660

Qy 661 ACAAGATCCCTTCATTGAGAGCGGGAGCGCGCTGCCCTCAAGCACATGGCTACTACC 720
 |||||||

Db 661 ACAAGATCCCTTCATTGAGAGCGGGAGCGCGCTGCCCTCAAGCACATGGCTACTACC 720

Qy 721 CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGCAACGCCAACCTCAGCTCCT 780
 |||||||

Db 721 CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGCAACGCCAACCTCAGCTCCT 780

Qy 781 CGGCCGCCCTCTCCAAGCGGGGGAGAAGGGAGACAAGTCGGTGGCAGTGGCGGG 840
 |||||||

Db 781 CGGCCGCCCTCTCCAAGCGGGGGAGAAGGGAGACAAGTCGGTGGCAGTGGCGGG 840

Qy 841 GCGGCCATGGGGCGGGCGGGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 |||||||

Db 841 GCGGCCATGGGGCGGGCGGGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

Qy 901 CGAGTGGCGCGCGCCAACTCCAACCGCGCAGAAAAGAGCTCGCGCTCAAAGTGG 960

Db	901	CGAGTGGCGCGCGCACA CTCAAACCGCGCAGAAAAAGCTCGCGCTCCAAAGTGG	960
Qy	961	CGGGCGCGCGGGGTGTTAGCAACCGCACGCCAAGCTATCTGGCAGGCCG	1020
Db	961	CGGGCGCGCGGGGTGTTAGCAACCGCACGCCAAGCTATCTGGCAGGCCG	1020
Qy	1021	GCGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCG	1080
Db	1021	GCGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCG	1080
Qy	1081	CCGCCGCCCTGCTGCCCTGGGCGCCGCCGACCACACTCGCTGTACAGGCCG	1140
Db	1081	CCGCCGCCCTGCTGCCCTGGGCGCCGCCGACCACACTCGCTGTACAGGCCG	1140
Qy	1141	CTCCCAGCGCCTCGGCCCTCCGCCCTCGCAGCCTCGGCCAGCGCTCGGCC	1200
Db	1141	CTCCCAGCGCCTCGGCCCTCCGCCCTCGCAGCCTCGGCCAGCGCTCGGCC	1200
Qy	1201	CGGGCAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCACTGTTCGGCGCC	1260
Db	1201	CGGGCAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCACTGTTCGGCGCC	1260
Qy	1261	CGTCGCTCGCCCGTGGCGCGTGGCGCGGAGCGGACCCCAGCGACCCCC	1320
Db	1261	CGTCGCTCGCCCGTGGCGCGTGGCGCGGAGCGGACCCCAGCGACCCCC	1320
Qy	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCCGACGCCAGCCTGAGCGCC	1380
Db	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCCGACGCCAGCCTGAGCGCC	1380
Qy	1381	GCGCCGCTCGTCCCCGCCGCCGCCCTCGCCGCCGACCCACGCCGCTACGCC	1440
Db	1381	GCGCCGCTCGTCCCCGCCGCCGCCCTCGCCGCCGACCCACGCCGCTACGCC	1440
Qy	1441	TGCGCGCCGCCTCGCCGCCCGTCCAGCGGCCCTCGCACCGCTCCCTCGC	1500
Db	1441	TGCGCGCCGCCTCGCCGCCCGTCCAGCGGCCCTCGCACCGCTCCCTCGC	1500
Qy	1501	CCCACTCTCTCTTCCCTCCCTCGGCCCTCTGTCTCCCGACGAGACTCGA	1560
Db	1501	CCCACTCTCTCTTCCCTCCCTCGGCCCTCTGTCTCCCGACGAGACTCGA	1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTCAGT	1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTCAGT	1620
Qy	1621	CGTCGCGCGCTCGACCGGGACCTGGATTAACTCGAGCCGGCTCCGCACT	1680
Db	1621	CGTCGCGCGCTCGACCGGGACCTGGATTAACTCGAGCCGGCTCCGCACT	1680
Qy	1681	TCGAGTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Db	1681	TCGAGTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Qy	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCGAGGCCAGGGAGAAGGGC	1800
Db	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCGAGGCCAGGGAGAAGGGC	1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAAGTGAAGAAAAGCAAAGGACAGACGAA	1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAAGTGAAGAAAAGCAAAGGACAGACGAA	1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAAAAGTAAGCAGGGCTCGTCCCGCGT	1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAAAAGTAAGCAGGGCTCGTCCCGCGT	1920

Qy	1921	TCTCGTCGCGGATCAAGGAGCGCGCCGGCTTGGACCCGCCTCCCATCCCCACCT	1980
Db	1921	TCTCGTCGCGGATCAAGGAGCGCGCCGGCTTGGACCCGCCTCCCATCCCCACCT	1980
Qy	1981	TCCCGGGCGGGGACCACACTGCCAGCGGGAGGGACCGGAGGAGGAAGAGGGTAGAC	2040
Db	1981	TCCCGGGCGGGGACCACACTGCCAGCGGGAGGGACCGGAGGAGGAAGAGGGTAGAC	2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAGCGAC	2100
Db	2041	AGGGCGACCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAGCGAC	2100
Qy	2101	TCAGTTGCTCCCTTGCTGAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Db	2101	TCAGTTGCTCCCTTGCTGAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Qy	2161	TTGCTGACCCCCAGCAAGAAGGGCAGTTAGTTCTAGAGACTTGAAGGAGCTCCCC	2220
Db	2161	TTGCTGACCCCCAGCAAGAAGGGCAGTTAGTTCTAGAGACTTGAAGGAGCTCCCC	2220
Qy	2221	CTTCTGCATCACCACTGGTTTATTGCTCTGGTCAAGAAAGGAGGGAA	2280
Db	2221	CTTCTGCATCACCACTGGTTTATTGCTCTGGTCAAGAAAGGAGGGAA	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGCTGATGAAGACAGAAGGCTCCGG	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGCTGATGAAGACAGAAGGCTCCGG	2340
Qy	2341	GGTACGAATTGGCGATGCCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC	2400
Db	2341	GGTACGAATTGGCGATGCCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC	2400
Qy	2401	GCAGCGAATTCCGTTGGGGCTTTTCTCCCTTTCCCCTGGCCCTCTGC	2460
Db	2401	GCAGCGAATTCCGTTGGGGCTTTTCTCCCTTTCCCCTGGCCCTCTGC	2460
Qy	2461	AGCGGAGGAGGAGATGTTGGGGAGGAGGCCAGCGTGTGACCGCGCTAGGAAATG	2520
Db	2461	AGCGGAGGAGGAGATGTTGGGGAGGAGGCCAGCGTGTGACCGCGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCCGTGGAGCCAGCAGCGGAGCTAGGGCGGGGGCGAGGAGGACA	2580
Db	2521	ACCCGAGAACCCCGTGGAGCCAGCAGCGGAGCTAGGGCGGGGGCGAGGAGGACA	2580
Qy	2581	CGAACTGGAAGGGGTTCACGGTCAAACCTGAAATGGATTGACGTTGGGAGCTGGCG	2640
Db	2581	CGAACTGGAAGGGGTTCACGGTCAAACCTGAAATGGATTGACGTTGGGAGCTGGCG	2640
Qy	2641	CGCGGCTGCTGGGCCTCCGCCTTCTACGTGAAATCAGTGAGGTGAGACTTCCCA	2700
Db	2641	CGCGGCTGCTGGGCCTCCGCCTTCTACGTGAAATCAGTGAGGTGAGACTTCCCA	2700
Qy	2701	GACCCGGAGGCGTGGAGGAGGAGACTGTTGATGTTGACAGGGCAGTCAGTGGAG	2760
Db	2701	GACCCGGAGGCGTGGAGGAGGAGACTGTTGATGTTGACAGGGCAGTCAGTGGAG	2760
Qy	2761	GGCAGTGGTTCCGAAAAAAAAAGAAAAAGGG	2797
Db	2761	GGCAGTGGTTCCGAAAAAAAAAGAAAAAGGG	2797

RESULT 5

ADA02535

ID ADA02535 standard; cDNA; 2797 BP.

XX

AC ADA02535;

XX

DT 11-JUN-2007 (revised)
 DT 06-NOV-2003 (first entry)
 XX
 DE Human SOX4 carcinoma associated cDNA, SEQ ID NO:1053.
 XX
 KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
 prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
 gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057146-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-US041414.
 XX
 PR 26-DEC-2001; 2001US-00035832.
 XX
 PA (SAGR-) SAGRES DISCOVERY.
 XX
 PI Morris DW;
 XX
 DR WPI; 2003-587068/55.
 DR PC:NCBI; gi36552.
 DR PC_ENCPRO:NCBI; gi36553.
 XX
 PT New recombinant nucleic acid encoding carcinoma associated protein,
 useful for preparing compositions for treating carcinomas.
 XX
 PS Claim 1; SEQ ID NO 1053; 245pp; English.
 XX
 CC The invention relates to recombinant carcinoma associated (CA) nucleic
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The
 CC invention also encompasses expression vectors and host cells comprising a
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
 binds to the protein, and a biochip comprising CA nucleic acid or
 fragments thereof. The sequences of the invention were identified using
 oncogenic retroviruses, which insert into the genome of the host organism
 at random. Many of these do not carry transduced host oncogenes or
 pathogenic trans-acting viral genes, meaning that cancer incidence is a
 direct consequence of the effects of proviral integration into host
 protooncogenes. The CA nucleic acid sequences can be used to diagnose
 carcinoma (especially breast cancer, prostate cancer, lymphoma or
 leukaemia) or a propensity to carcinoma by determination of the sequence
 of a CA gene, or by determination of CA gene expression in particular
 tissues. CA nucleic acids, proteins and antibodies are also useful as
 therapeutic agents and in screening and evaluating drug candidates. The
 present sequence represents a specifically claimed human CA nucleic acid
 sequence of the invention. Note: The complete sequence data for this
 patent did not form part of the printed specification, but was obtained
 in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 information from BOND.
 XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 9; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTCCCCAGATTCGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG	60
Db	1	TTCCCCAGATTCGAGAAAATCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG	60

Qy	61	ACAGCAAACCTGCAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120
Db	61	ACAGCAAACCTGCAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120
Qy	121	GGAACATAACTCCTCTCGAGAGGGCGAGAACTCCTCCCCAATCTTTGGGACTTT 180
Db	121	GGAACATAACTCCTCTCGAGAGGGCGAGAACTCCTCCCCAATCTTTGGGACTTT 180
Qy	181	TCTCTTTACCCACCTCCGCCCTCGAGGAGTTGAGGGCCAGTCGGCGCGCG 240
Db	181	TCTCTTTACCCACCTCCGCCCTCGAGGAGTTGAGGGCCAGTCGGCGCGCG 240
Qy	241	CGTCTCCCGTTCGGCGTGTCTTGGCCGGGAACCGGGAGGGCCGGCATCCGGG 300
Db	241	CGTCTCCCGTTCGGCGTGTCTTGGCCGGGAACCGGGAGGGCCGGCATCCGGG 300
Qy	301	CGGCCGCGAGGGTGTGAGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTCAGC 360
Db	301	CGGCCGCGAGGGTGTGAGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTCAGC 360
Qy	361	AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCCGGAGAGCTCGGACTCGGGG 420
Db	361	AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCCGGAGAGCTCGGACTCGGGG 420
Qy	421	CGGGCTCTGAGCTGGGAATCGCCTCCTCCCCACGCCGGCTCACGCCCTCACGGGG 480
Db	421	CGGGCTCTGAGCTGGGAATCGCCTCCTCCCCACGCCGGCTCACGCCCTCACGGGG 480
Qy	481	GCAAGGCCGACGACCCGAGCTGGTCAAGACCCCAGTGGGCACATCAAGGCCATGA 540
Db	481	GCAAGGCCGACGACCCGAGCTGGTCAAGACCCCAGTGGGCACATCAAGGCCATGA 540
Qy	541	ACGCCCTCATGGTGTGGTCAGATCGAGGCCGCAAGATCATGGAGCAGTCGGCCGACA 600
Db	541	ACGCCCTCATGGTGTGGTCAGATCGAGGCCGCAAGATCATGGAGCAGTCGGCCGACA 600
Qy	601	TGCACAACGCCGAGATCTCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Db	601	TGCACAACGCCGAGATCTCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Qy	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCGCTGCGCTCAAGCACATGGCTGACTACC 720
Db	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCGCTGCGCTCAAGCACATGGCTGACTACC 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACCTCCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACCTCCAGCTCT 780
Qy	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGAACAGTCGCGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGAACAGTCGCGTGGCAGTGGCGGG 840
Qy	841	GCGGCATGGGGCGCGCGCGCGCGGGAGCAGCAACCGGGGGAGGAGGCCGGT 900
Db	841	GCGGCATGGGGCGCGCGCGCGGGAGCAGCAACCGGGGGAGGAGGCCGGT 900
Qy	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Db	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Qy	961	CGGGCGGCCGGGGCTGGGGTAGCAAACCGCAGCCAAGCTCATCTGGCAGGCCG 1020
Db	961	CGGGCGGCCGGGGCTGGGGTAGCAAACCGCAGCCAAGCTCATCTGGCAGGCCG 1020
Qy	1021	CGGGCGGCCGGGAAGCAGCGCTGCCGCCGCTCTCGCCCGAACAGCGGGGG 1080
		CGGGCGGCCGGGAAGCAGCGCTGCCGCCGCTCTCGCCCGAACAGCGGGGG 1080

Db	1021	CGGGCGCGGGAAAGCAGCGGTGCGCCGCCCTTCGCCGCCAACAGGGGGGG 1080
Qy	1081	CGCCGCCCTGCTGCCCTGGGCAGCCGCCGACCACACTCGCTGTACAAGGGGG 1140
Db	1081	CGCCGCCCTGCTGCCCTGGGCAGCCGCCGACCACACTCGCTGTACAAGGGGG 1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCGGCAGCCGCCGACCACACTCGCTGTACAAGGGGG 1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCGGCAGCCGCCGACCACACTCGCTGTACAAGGGGG 1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGTCACTTGTGGCCCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGTCACTTGTGGCCCTGGCA 1260
Qy	1261	CGTCGTCGCCGTGGCGCGTGGCGCGGAGCCGACCCAGCGACCCCTGGCC 1320
Db	1261	CGTCGTCGCCGTGGCGCGTGGCGCGGAGCCGACCCAGCGACCCCTGGCC 1320
Qy	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCAGCGCCGCCAGCTGAGCGCCCG 1380
Db	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCAGCGCCGCCAGCTGAGCGCCCG 1380
Qy	1381	GCGCCGCTCGTCCCCGCCGCCGCCGCTGCCGCCGACCCACGCCAGCC 1440
Db	1381	GCGCCGCTCGTCCCCGCCGCCGCCGCTGCCGCCGACCCACGCCAGCC 1440
Qy	1441	TGCGGCCGCGCTCGCCGCCCGTCAAGCGCCCTCGCACCGTCCCTCGGCTCGT 1500
Db	1441	TGCGGCCGCGCTCGCCGCCCGTCAAGCGCCCTCGCACCGTCCCTCGGCTCGT 1500
Qy	1501	CCCACTCCCTCTTCCTCCCTCGGGCTCTCGTCCCGACGACGAGTTCGAAGACG 1560
Db	1501	CCCACTCCCTCTTCCTCCCTCGGGCTCTCGTCCCGACGACGAGTTCGAAGACG 1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTTCAGTT 1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTTCAGTT 1620
Qy	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTTCAGCGCCGGCTCCGCACT 1680
Db	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTTCAGCGCCGGCTCCGCACT 1680
Qy	1681	TCGAGTTCCCGGACTACTGCACGCCGGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Db	1681	TCGAGTTCCCGGACTACTGCACGCCGGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Qy	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAAGGGCGCGAGCAGGGAGAAGGGC 1800
Db	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAAGGGCGCGAGCAGGGAGAAGGGC 1800
Qy	1801	CGGGGGGGTAGGAGAGGAAAAAAAAGTGAAGGGAGACAGCAA 1860
Db	1801	CGGGGGGGTAGGAGAGGAAAAAAAAGTGAAGGGAGACAGCAA 1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAAGAAAAGTAAGCAGGGCTCGTTCGCCCGCT 1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAAGAAAAGTAAGCAGGGCTCGTTCGCCCGCT 1920
Qy	1921	TCTCGTCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT 1980
Db	1921	TCTCGTCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT 1980
Qy	1981	TCCCCGGCGGGGACCCACTCTGCCAGCCGGAGGGACCGGGAGGAGGAAGAGGGTAGAC 2040
Db	1981	TCCCCGGCGGGGACCCACTCTGCCAGCCGGAGGGACCGGGAGGAGGAAGAGGGTAGAC 2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAGCGAC 2100

RESULT

ADH28813

TR ADH28813 standard: DNA: 2797 BP.

xx

AC ADH28813:

xx

AA
DT 11-JUN-2007 (revised)
DT 11-MAR-2004 (first entry)

xx

DE Human chronic myelogenous leukaemia (CML) gene marker #81

xx

KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myclogenous leukaemia

KW gene marker.

xx

OS Homo sapiens.
 XX
 PN US2003104426-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 14-JUN-2002; 2002US-00171581.
 XX
 PR 18-JUN-2001; 2001US-0298914P.
 XX
 PA (LINS/) LINSLEY P S.
 PA (MAOM/) MAO M.
 PA (DAIH/) DAI H.
 PA (HEYD/) HE Y.
 PA (RADJ/) RADICH J P.
 XX
 PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
 XX
 DR WPI; 2003-787046/74.
 DR PC:NCBI; gi36552.
 DR PC_ENCPRO:NCBI; gi36553.
 XX
 PT Classifying cell sample as chronic phase chronic myelogenous leukemia or
 PT blast crisis chronic myelogenous leukemia by detecting difference in
 PT expression of genes corresponding to the markers such as X15415, U89436.
 XX
 PS Disclosure; SEQ ID NO 81; 31pp; English.
 XX
 CC The invention relates to a method of classifying a cell sample as chronic
 CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-
 CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.
 CC The present sequence represents a human chronic myelogenous leukaemia
 CC (CML) gene marker used to distinguish blast crisis CML from chronic phase
 CC CML.
 CC
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

 Query Match 100.0%; Score 2797; DB 10; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 TCCCCAGATTGAGAAAATCCTCTCTACTTACGACGGTCTCCAGACTCAGCCGAGAG 60
 |||||||
 Db 1 TCCCCAGATTGAGAAAATCCTCTCTACTTACGACGGTCTCCAGACTCAGCCGAGAG 60

 Qy 61 ACAGCAAATCTGAGCGCGGTGAGAGGCGAGAGAGAGGGAGAGAGACTCTCCAGCCTG 120
 |||||||
 Db 61 ACAGCAAATCTGAGCGCGGTGAGAGGCGAGAGAGAGGGAGAGAGACTCTCCAGCCTG 120

 Qy 121 GGAACTATAACTCCTCTGCAGAGGCCGAGAACTCCTCCCCAAATCTTTGGGACTTT 180
 |||||||
 Db 121 GGAACTATAACTCCTCTGCAGAGGCCGAGAACTCCTCCCCAAATCTTTGGGACTTT 180

 Qy 181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGGCAGTTCGGCCGCCGCCG 240
 |||||||
 Db 181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGGCAGTTCGGCCGCCGCCG 240

 Qy 241 CGTCTCCCGTTCGGCGTGTGCTTGGCCCGGGAACCGGGAGGGCCGGCATCGCGCG 300
 |||||||
 Db 241 CGTCTCCCGTTCGGCGTGTGCTTGGCCCGGGAACCGGGAGGGCCGGCATCGCGCG 300

 Qy 301 CGGCCGCCGCGAGGGTGTGAGCGCGCTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360
 |||||||
 Db 301 CGGCCGCCGCGAGGGTGTGAGCGCGCTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360

Qy	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGCAGAGCTCGGACTCGGGCG 420
Db	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGCAGAGCTCGGACTCGGGCG 420
Qy	421	CCGGCCTCGAGCTGGGAATGCCCTCCCCACGCCGGCTCCACGCCCTCACGGGGCG 480
Db	421	CCGGCCTCGAGCTGGGAATGCCCTCCCCACGCCGGCTCCACGCCCTCACGGGGCG 480
Qy	481	GCAAGGCCGACGCCGAGCTGGTCAAGACCCCCGAGTGCGGACATCAAGGCCCATGA 540
Db	481	GCAAGGCCGACGCCGAGCTGGTCAAGACCCCCGAGTGCGGACATCAAGGCCCATGA 540
Qy	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGCCGCAAGATCATGGAGCAGTCGGCGGACA 600
Db	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGCCGCAAGATCATGGAGCAGTCGGCGGACA 600
Qy	601	TGCACAACGCCGAGATCTCCAAGCGGCTGGCAAACGCTGGAAGCTGCTAAAGACAGCG 660
Db	601	TGCACAACGCCGAGATCTCCAAGCGGCTGGCAAACGCTGGAAGCTGCTAAAGACAGCG 660
Qy	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCAGCTGGCTGCGCTCAAGCACATGGCTGACTACC 720
Db	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCAGCTGGCTGCGCTCAAGCACATGGCTGACTACC 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Qy	781	CGGCCGCCGCCTCCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCGCCTCCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG 840
Qy	841	CGGCCATGGGGCGGGCGGGCGGGAGGAGGAGACAAGGGGGAGAGGGAGCGCGGTG 900
Db	841	CGGCCATGGGGCGGGCGGGAGGAGACAAGGGGGAGAGGGAGCGCGGTG 900
Qy	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Db	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Qy	961	CGGGCGGCCGGCGGGCGGTGGGGTAGCAAACCGCACGCCAACCTCATCTGGCAGGCCG 1020
Db	961	CGGGCGGCCGGCGGTGGGGTAGCAAACCGCACGCCAACCTCATCTGGCAGGCCG 1020
Qy	1021	CGGGCGGCCGGAAAGCACGCCGCTGCCGCCGCCCTCTGCCGCCAACAGGGGGGG 1080
Db	1021	CGGGCGGCCGGAAAGCACGCCGCTGCCGCCGCCCTCTGCCGCCAACAGGGGGGG 1080
Qy	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Db	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCCGCCAGCCTGCCCTCCGCCAGCCTGCC 1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCCGCCAGCCTGCCCTCCGCCAGCCTGCC 1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTCACCTGTTGGCGGCCCTGGCGA 1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTCACCTGTTGGCGGCCCTGGCGA 1260
Qy	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCCGGAGCCGACCCAGCGACCCCTGGCG 1320
Db	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCCGGAGCCGACCCAGCGACCCCTGGCG 1320
Qy	1321	TGTACGGAGGAGGGAGGCCGCCCTGCTGCCCGAGCGCCAGCCCTGAGCGGCCAGCGA 1380

Db	1321	TGTACGAGGAGGGCGCGGGCTGCTCGCCGAGCAGCCCAGCTGAGCGCCGAGCA	1380
Qy	1381	GCGCCGCCCTGCTCCCCCGCCGCCGCGCTCGCCCGCCGACCACCGCGCTACGCCAGCC	1440
Db	1381	GCGCCGCCCTGCTCCCCCGCCGCCGCGCTCGCCCGCCGACCACCGCGCTACGCCAGCC	1440
Qy	1441	TGCGCGCCGCCCTCGCCCCCGCCGCCGCGCTCGCCCGCCGACCACCGCGCTCGGCCTCGT	1500
Db	1441	TGCGCGCCGCCCTCGCCCCCGCCGCCGCGCTCGCCCGCCGACCACCGCGCTCGGCCTCGT	1500
Qy	1501	CCCACTCCCTCTCCCTCCCTCGGGCTCTCGTCCCTCCGACGACGAGTCGAAGACG	1560
Db	1501	CCCACTCCCTCTCCCTCCCTCGGGCTCTCGTCCCTCCGACGACGAGTCGAAGACG	1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAACTTGAGAGCATGTCCTGGCAGCTCAGTT	1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAACTTGAGAGCATGTCCTGGCAGCTCAGTT	1620
Qy	1621	CGTCGTCGGCGCTGACCGGGACCTGGATTAACTTCGAGCCGGCTCCGGCTCGCACT	1680
Db	1621	CGTCGTCGGCGCTGACCGGGACCTGGATTAACTTCGAGCCGGCTCCGGCTCGCACT	1680
Qy	1681	TCGAGTTCCCGGACTACTGACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Db	1681	TCGAGTTCCCGGACTACTGACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Qy	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAGGGCGGCAGGCAGGGAGAAGGGC	1800
Db	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAGGGCGGCAGGCAGGGAGAAGGGC	1800
Qy	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGACAGACGAA	1860
Db	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGACAGACGAA	1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAAAGTAAGCAGGGCTCGTTCGCCCGGT	1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAAAGTAAGCAGGGCTCGTTCGCCCGGT	1920
Qy	1921	TCTCGTCGCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT	1980
Db	1921	TCTCGTCGCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT	1980
Qy	1981	TCCCGGGCGGGGACCACTCTGCCACGCCGGGAGGGACCGGGAGGGAGAGGGTAGAC	2040
Db	1981	TCCCGGGCGGGGACCACTCTGCCACGCCGGGAGGGACCGGGAGGGAGAGGGTAGAC	2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGTGTTGATGCCAAAAAAAGCGAC	2100
Db	2041	AGGGCGACCTGTGATTGTTATTGTGTTGATGCCAAAAAAAGCGAC	2100
Qy	2101	TTCGAGTTGCTCCCTTGCTGAGAGACCCCTCCCCCTCCAACGAGCTCCGGAC	2160
Db	2101	TTCGAGTTGCTCCCTTGCTGAGAGACCCCTCCCCCTCCAACGAGCTCCGGAC	2160
Qy	2161	TTGTCGACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTGAGAGACTCTCCC	2220
Db	2161	TTGTCGACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTGAGAGACTCTCCC	2220
Qy	2221	CTTCCCTGCATCACCACTTGGTTTATTTGCTTCTGGTCAGAAAGGAGGGGA	2280
Db	2221	CTTCCCTGCATCACCACTTGGTTTATTTGCTTCTGGTCAGAAAGGAGGGGA	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCCTTTTAAACCGCGTGTGAAGACAGAAGGCTCCGG	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCCTTTTAAACCGCGTGTGAAGACAGAAGGCTCCGG	2340
Qy	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC	2400

Db	2341	GGTGACGAATTGGCCATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Qy	2401	GCAGCGAATTCCTTGGGCTTTCTCCCTCTTCCCCTGCCCCCTCTGC	2460
Db	2401	GCAGCGAATTCCTTGGGCTTTCTCCCTCTTCCCCTGCCCCCTCTGC	2460
Qy	2461	AGCCGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Db	2461	AGCCGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGAGCTAGGGCGGGCGAGGAGGACA	2580
Db	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGAGCTAGGGCGGGCGAGGAGGACA	2580
Qy	2581	CGAACTGGAAGGGGTTACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Db	2581	CGAACTGGAAGGGGTTACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Qy	2641	CGGGGGCTGCTGGGCCTCCGCCTCTTACGTGAAATCAGTGAGGTGAGACTTCCA	2700
Db	2641	CGGGGGCTGCTGGGCCTCCGCCTCTTACGTGAAATCAGTGAGGTGAGACTTCCA	2700
Qy	2701	GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Db	2701	GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Qy	2761	GGCGAGTGGTTCGGAAAAAAAAAAAAAGAAAAAAAGGG 2797	
Db	2761	GGCGAGTGGTTCGGAAAAAAAAAAAAAGAAAAAAAGGG 2797	

RESULT 7

ACN38485

ID ACN38485 standard; cDNA; 2797 BP.

XX

AC ACN38485;

XX

DT 11-JUN-2007 (revised)
DT 18-NOV-2004 (first entry)

XX

DE Tumour-associated antigenic target (TAT) cDNA DNA290785, SEQ ID NO:2032.

XX

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.

XX

OS Homo sapiens.

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PN WO2004030615-A2.

XX

PD 15-APR-2004.

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PF 29-SEP-2003; 2003WO-US028547.

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PR 02-OCT-2002; 2002US-0414971P.

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PA (GETH) GENENTECH INC.

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PI Wu TD, Zhang Z, Zhou Y;

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DR WPI; 2004-347921/32.

DR P-PSDB; ABM80791.

DR PC:NCBI; gi36552.

DR PC_ENCPRO:NCBI; gi36553.

XX

PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX

PS Claim 1; SEQ ID NO 2032; 7273pp; English.

XX

CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 12; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCCCCAGCAATTGAGAAACTCTCTCTACTTTAGCACGGGTCTCAGACTCAGCCGAGAG 60
 |||||||

Db 1 TTCCCCCAGCAATTGAGAAACTCTCTCTACTTTAGCACGGGTCTCAGACTCAGCCGAGAG 60

Qy 61 ACAGCAAACCTGCAGCGCGGTGAGAGAGCAGAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120

Db 61 ACAGCAAACCTGCAGCGCGGTGAGAGAGCAGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120

Qy 121 GGAACATAACTCTCTCGAGAGGGCGAGAACCTCTCCCAAATCTTTGGGACTTT 180

Db 121 GGAACATAACTCTCTCGAGAGGGCGAGAACCTCTCCCAAATCTTTGGGACTTT 180

Qy 181 TCTCTCTTACCCACCTCCGCCCTCGCAGGGAGTGAGGGGCCAGTTCGGCCGCCGCC 240

Db 181 TCTCTCTTACCCACCTCCGCCCTCGCAGGGAGTGAGGGGCCAGTTCGGCCGCCGCC 240

Qy 241 CGTCTCCCGTTCGGCGTGTGCTTGCGCCGGGAACCGGGAGGGCCCGCATCGCGCG 300

Db 241 CGTCTCCCGTTCGGCGTGTGCTTGCGCCGGGAACCGGGAGGGCCCGCATCGCGCG 300

Qy 301 CGGCCGCCGAGGGTGTGAGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360

Db 301 CGGCCGCCGAGGGTGTGAGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTGCAGC 360

Qy 361 AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCGCCGAGAGCTCGACTCGGGC 420

Db 361 AAACCAACAATGCCAGAACCGGAAGCGCTGCTGGCGCCGAGAGCTCGACTCGGGC 420

Qy	421	CCGGCCTCGAGCTGGGAATCGCCTCTCCCCACGCCGGCTCCACCGCTCCACGGCG 480
Db	421	CCGGCCTCGAGCTGGGAATCGCCTCTCCCCACGCCGGCTCCACCGCTCCACGGCG 480
Qy	481	GCAAGGCGGACGACCCGAGCTGGTCAAGACCCCAGTGGGCACATCAAGGGACCCATGA 540
Db	481	GCAAGGCGGACGACCCGAGCTGGTCAAGACCCCAGTGGGCACATCAAGGGACCCATGA 540
Qy	541	ACGCCTTCATGGTGTTGTCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCGACA 600
Db	541	ACGCCTTCATGGTGTTGTCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCGACA 600
Qy	601	TGCACAAACGCCGAGATCTCCAAGCGGCTGGCAAACCGTGGAAAGCTGCTCAAAGACAGCG 660
Db	601	TGCACAAACGCCGAGATCTCCAAGCGGCTGGCAAACCGTGGAAAGCTGCTCAAAGACAGCG 660
Qy	661	ACAAGATCCTTTCATTGAGAGGCCAGGAGAAGGGTGAAGTCGCCAACGCCAACTCCAGCTCT 720
Db	661	ACAAGATCCTTTCATTGAGAGGCCAGGAGAAGGGTGAAGTCGCCAACGCCAACTCCAGCTCT 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGCCAACGCCAACTCCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGCCAACGCCAACTCCAGCTCT 780
Qy	781	CGGCCGCCGCCCTCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCGCCCTCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGG 840
Qy	841	CGGCCCATGGGGCGGCCGGCGCGCGCGGGAGCAGCAACCGGGGGAGGAGGCCGGT 900
Db	841	CGGCCCATGGGGCGGCCGGCGCGCGGGAGCAGCAACCGGGGGAGGAGGCCGGT 900
Qy	901	CGAGTGGCGGGGCCCAACTCCAACCGGCCAGAAAAAAAGCTGCCCTCAAAGTGG 960
Db	901	CGAGTGGCGGGGCCCAACTCCAACCGGCCAGAAAAAAAGCTGCCCTCAAAGTGG 960
Qy	961	CGGGCGCGCGGGCGGTGGGTTAGCAAACCGCACGCCAGCTCATCCTGGCAGGCCG 1020
Db	961	CGGGCGCGCGGGCGGTGGGTTAGCAAACCGCACGCCAGCTCATCCTGGCAGGCCG 1020
Qy	1021	CGGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGGGG 1080
Db	1021	CGGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGGGG 1080
Qy	1081	CCGCCCTCTGCCGCCCTGGGCCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Db	1081	CCGCCCTCTGCCGCCCTGGGCCGCCGCCGACCACACTCGCTGTACAAGGCCGGA 1140
Qy	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCTGGCAGCTCGCCCTCCGAGCGCTCGGGCCC 1200
Db	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCTGGCAGCTCGCCCTCCGAGCGCTCGGGCCC 1200
Qy	1201	CGGGCAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCACTGTGGCGGCCCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCACTGTGGCGGCCCTGGCA 1260
Qy	1261	CGTCGTCGCGCCGTGGCGCGTGGCGCGGGAGCCGACCCAGCGACCCCTGGCC 1320
Db	1261	CGTCGTCGCGCCGTGGCGCGTGGCGCGGGAGCCGACCCAGCGACCCCTGGCC 1320
Qy	1321	TGTACGAGGAGGGAGGGCGGGCTGCTGCCAGCGCCGGACGCCCTGAGCGCCGAGCA 1380
Db	1321	TGTACGAGGAGGGAGGGCGGGCTGCTGCCAGCGCCGGACGCCCTGAGCGCCGAGCA 1380
Qy	1381	CGCCGCCCTCGTCCCCCGCCGCCGGCCCTGCCGCCGACCCAGCGACCCCTGGCC 1440

Db	1381	GCGCCGCCCTCGCCCCCGCCGGCCGCTGCCGCCGACCCAGCAGCTACGCCAGCC 1440
Qy	1441	TGCGCCGCCCTGCCGCCGCCCTGCCAGCGGCCCTCGCACCGTCCCTCCCTCGGCCTCGT 1500
Db	1441	TGCGCCGCCCTGCCGCCGCCCTGCCAGCGGCCCTCGCACCGTCCCTCCCTCGGCCTCGT 1500
Qy	1501	CCCACTCTCTCTCTCCCTCCCTCGGCTCCTCGTCTCCCGACGACGAGTCGAAGACG 1560
Db	1501	CCCACTCTCTCTCTCCCTCCCTCGGCTCCTCGTCTCCCGACGACGAGTCGAAGACG 1560
Qy	1561	ACCTGCTGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGCAGCTTCAGTT 1620
Db	1561	ACCTGCTGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGCAGCTTCAGTT 1620
Qy	1621	CGTCGCGGCGTCGACCGGACCTGGATTTAACTCGAGCCGGCTCCGGCTCGCACT 1680
Db	1621	CGTCGCGGCGTCGACCGGACCTGGATTTAACTCGAGCCGGCTCCGGCTCGCACT 1680
Qy	1681	TCGAGTTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Db	1681	TCGAGTTCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Qy	1741	AGTCACGATCTCAACCTGGTTTACCTACTGAAGGGCCGCAGGCAGGGAGAACGGC 1800
Db	1741	AGTCACGATCTCAACCTGGTTTACCTACTGAAGGGCCGCAGGCAGGGAGAACGGC 1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAAAAAAGAAACGAAAAGGACAGACGAA 1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAGTGAAAAAAAGAAACGAAAAGGACAGACGAA 1860
Qy	1861	GAGTTAAAGGAGAAAGGAGAAAAGAAAAGTAAGCAGGGCTCGTCGCCCGCGT 1920
Db	1861	GAGTTAAAGGAGAAAGGAGAAAAGAAAAGTAAGCAGGGCTCGTCGCCCGCGT 1920
Qy	1921	TCTCGTCGGATCAAGGAGCCGCCGCGTTTGACCCGCTCCCATCCCCACCT 1980
Db	1921	TCTCGTCGGATCAAGGAGCCGCCGCGTTTGACCCGCTCCCATCCCCACCT 1980
Qy	1981	TCCCGGGCGGGGACCCACTCTGCCACGCCGAGGGACCGGGAGGAGAAAGGGTAGAC 2040
Db	1981	TCCCGGGCGGGGACCCACTCTGCCACGCCGAGGGACCGGGAGGAGAAAGGGTAGAC 2040
Qy	2041	AGGGCGCAGCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAAAGCGAC 2100
Db	2041	AGGGCGCAGCTGTGATTGTTATTGATGTTGTTGATGGCAAAAAAAAAAGCGAC 2100
Qy	2101	TTCGAGTTGCTCCCTTGTGTAAGGAGCCCCCTCCCTTCCAACGAGCTCGGAC 2160
Db	2101	TTCGAGTTGCTCCCTTGTGTAAGGAGCCCCCTCCCTTCCAACGAGCTCGGAC 2160
Qy	2161	TTGTCGACCCCCAGACAAGGGCAGTTAGTTCTAGAGACTTGAAGGAGCTCCCC 2220
Db	2161	TTGTCGACCCCCAGACAAGGGCAGTTAGTTCTAGAGACTTGAAGGAGCTCCCC 2220
Qy	2221	CTTCCTGCATACCACCTGGTTTATTGCTCTGGTCAAGAAAGGAGGGGA 2280
Db	2221	CTTCCTGCATACCACCTGGTTTATTGCTCTGGTCAAGAAAGGAGGGGA 2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCCTTTTAAACCGGTGATGAAGACAGAAGGCTCGG 2340
Db	2281	GAACCCAGCGCACCCCTCCCCCCTTTTAAACCGGTGATGAAGACAGAAGGCTCGG 2340
Qy	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Db	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Qy	2401	GCAGGCGAATCCGTTGGGCCTTTTCCCTCCCTTCCCCCTCTGC 2460

Db	2401	GCAGGGCAATTCCCGTTGGGGCTTTTCCCTCCCTTTCCCTGGCCCCCTGC	2460
Qy	2461	AGCGGAGGAGGAGATGTTGAGGGAGGCCAGCCAGTGACCGCGCTAGGAAATG	2520
Db	2461	AGCGGAGGAGGAGATGTTGAGGGAGGCCAGCCAGTGACCGCGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGGACTAGGGCGGGGCGAGGAGACA	2580
Db	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGGACTAGGGCGGGGCGAGGAGACA	2580
Qy	2581	CGAACTGGAAGGGGTTACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Db	2581	CGAACTGGAAGGGGTTACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Qy	2641	CGGCGGCTGCTGGGCCCTCCGCCTTCTACGTGAAATCAGTGAGGTGAGACTTCCC	2700
Db	2641	CGGCGGCTGCTGGGCCCTCCGCCTTCTACGTGAAATCAGTGAGGTGAGACTTCCC	2700
Qy	2701	GACCCGGAGGCCTGGAGGAGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Db	2701	GACCCGGAGGCCTGGAGGAGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Qy	2761	GGCGAGTGGTTCGAAAAAAAAGAAAAAAAGGG	2797
Db	2761	GGCGAGTGGTTCGAAAAAAAAGAAAAAAAGGG	2797

RESULT 8
 ADW47984
 ID ADW47984 standard; cDNA; 2797 BP.
 XX
 AC ADW47984;
 XX
 DT 11-JUN-2007 (revised)
 DT 07-APR-2005 (first entry)
 XX
 DE Human sex determining region Y box 4 (SOX4) nucleic acid.
 XX
 KW Sex determining region Y box 4; SOX4; prostate tumor; cytostatic;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 351..1775
 FT /*tag= a
 FT /product= "Human SOX4"
 XX
 PN WO2005007830-A2.
 XX
 PD 27-JAN-2005.
 XX
 PF 14-JUL-2004; 2004WO-US022850.
 XX
 PR 14-JUL-2003; 2003US-0487553P.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX
 PI Vanaja DK, Young CYF;
 XX
 DR WPI; 2005-102097/11.
 DR P-PSDB; ADW47985.
 DR PC:NCBI; gi36552.
 DR PC_ENCPRO:NCBI; gi36553.
 XX
 PT Detecting/detecting and distinguishing between or among prostate cell

PT proliferative disorders or their stages in a subject, useful for treating
 PT prostate cancer, by determining gene expression level of e.g. supervillin
 PT (SIVL).

XX
 PS Claim 1; SEQ ID NO 43; 178pp; English.

CC The invention provides novel methods and compositions for the diagnosis,
 CC staging and prognosis of prostate cancer based on DNA methylation and/or
 CC modulation of gene expression, including transcriptional silencing. Gene
 CC expression profiling in benign and untreated human prostate cancer
 CC tissues identified diagnostic and/or prognostic nucleic acid and protein
 CC markers. These included: the differentially (relative to benign tissue)
 CC down-regulated sequences corresponding to zinc finger protein 185
 CC (ZNF185), prostate secretory protein (PSP94), bulbous pemphigoid antigen
 CC (BPAG), supervillin (SIVL), proline rich membrane anchor 1 (PRIMA1),
 CC TU3A, FLJ14084, KIAA 1210, Sorbin and SH3 domain containing 1 (SORBS1),
 CC and C2orf63; and the differentially up-regulated sequences MARCKS-like
 CC protein (MLP), SRY (sex determining region Y)-box 4 (SOX4), fatty acid
 CC binding protein 5 (FABP5), MAL2 and Erg isoform 2 (erg-2). Also provided
 CC are nucleic acids, nucleic acid arrays and kits useful for detecting, or
 CC for detecting and differentiating between or among prostate cell
 CC proliferative disorders and/or tumor progression. The present sequence is
 CC that of a polynucleotide encoding human SOX4, a high mobility group box 4
 CC transcription factor involved in the regulation of embryonic development
 CC and in the determination of cell fate. Increase of SOX4 levels indicates
 CC a role in development and/or progression of prostate cancer.
 CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 16; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 TTCCCCCAGCATCGAGAAACTCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Db	1 TTCCCCCAGCATCGAGAAACTCCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG 60
Qy	61 ACAGCAAACCTGCAGCGCGGTGAGAGAGCGAGAGAGGGAGAGAGAGACTCTCCAGCCTG 120
Db	61 ACAGCAAACCTGCAGCGCGGTGAGAGAGCGAGAGAGGGAGAGAGAGACTCTCCAGCCTG 120
Qy	121 GGAACATAACTCCTCTCGAGAGGGCGAGAACTCTCCCAAAATCTTTGGGACTTT 180
Db	121 GGAACATAACTCCTCTCGAGAGGGCGAGAACTCTCCCAAAATCTTTGGGACTTT 180
Qy	181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGCCAGTTGGCCGCCGCG 240
Db	181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGGCCAGTTGGCCGCCGCG 240
Qy	241 CGTCTCCCGTTCGGCGTGTCTGGCCCGGGGAAACGGGAGGGCCGGCATCGCGGG 300
Db	241 CGTCTCCCGTTCGGCGTGTCTGGCCCGGGAAACGGGAGGGCCGGCATCGCGGG 300
Qy	301 CGGCCGCCGAGGGTGAGCGCCGCTGGCGCCGCCGAGCCGAGGGCATGGTGCAGC 360
Db	301 CGGCCGCCGAGGGTGAGCGCCGCTGGCGCCGCCGAGCCGAGGGCATGGTGCAGC 360
Qy	361 AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGCCGAGAGCTGGACTCGGGC 420
Db	361 AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGCCGAGAGCTGGACTCGGGC 420
Qy	421 CGGCCCTCGAGCTGGGAATGCCCTCTCCCCACGCCGCCGCTCCACGCCCTCCACGGG 480
Db	421 CGGCCCTCGAGCTGGGAATGCCCTCTCCCCACGCCGCCGCTCCACGCCCTCCACGGG 480

Qy	481	GCAAGGCCGACGCCGGAGCTGGTCAAGACCCCGAGTGGCACATCAAGCGACCCATGA 540
Db	481	GCAAGGCCGACGCCGGAGCTGGTCAAGACCCCGAGTGGCACATCAAGCGACCCATGA 540
Qy	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGGCAGAGATCATGGAGCAGTCGCCGACA 600
Db	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGGCAGAGATCATGGAGCAGTCGCCGACA 600
Qy	601	TGCACAACGCCGAGATCTCAAGCGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Db	601	TGCACAACGCCGAGATCTCAAGCGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Qy	661	ACAAGATCCCTTCATTGAGAGGCGGAGCGCCTCGCCTCAAGCACATGGTACTACC 720
Db	661	ACAAGATCCCTTCATTGAGAGGCGGAGCGCCTCGCCTCAAGCACATGGTACTACC 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Qy	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGTCGGTGCAGTGGCGGGG 840
Db	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGTCGGTGCAGTGGCGGGG 840
Qy	841	GCGGCATGGGGCGCCGGCGCCGGCGGGAGCAGCAACCGGGGGAGGAGCGCGGTG 900
Db	841	GCGGCATGGGGCGCCGGCGCCGGCGGGAGCAGCAACCGGGGGAGGAGCGCGGTG 900
Qy	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAAGAGCTGCGCTCAAAGTGG 960
Db	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAAGAGCTGCGCTCAAAGTGG 960
Qy	961	CGGGCGGCCGGCGGTGGGTTAGCAAACCCGACGCCAACGCTCATCTGGCAGCGCCG 1020
Db	961	CGGGCGGCCGGCGGTGGGTTAGCAAACCCGACGCCAACGCTCATCTGGCAGCGCCG 1020
Qy	1021	CGGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGCGGGGGG 1080
Db	1021	CGGGCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGCGGGGGG 1080
Qy	1081	CCGCCGCCCTGCTGCCCTGGGCCGCCGCCGACCAACTCGCTGTACAAGGCGCGGA 1140
Db	1081	CCGCCGCCCTGCTGCCCTGGGCCGCCGCCGACCAACTCGCTGTACAAGGCGCGGA 1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCGGCAGCCTGCCCTCCGCCAGCGCTCGGGCC 1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCGGCAGCCTGCCCTCCGCCAGCGCTCGGGCC 1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGCTACCTGTTGCCGCCCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGCTACCTGTTGCCGCCCTGGCA 1260
Qy	1261	CGTCGCTGCCCTGGCGCGCTGGCGCGGGAGCGACCCAGCGACCCCTGGGCC 1320
Db	1261	CGTCGCTGCCCTGGCGCGCTGGCGCGGGAGCGACCCAGCGACCCCTGGGCC 1320
Qy	1321	TGTACGAGGAGGAGGGCGGGCTGCCGCCAGCGCCAGCCTGAGCGGCCAGCA 1380
Db	1321	TGTACGAGGAGGAGGGCGGGCTGCCGCCAGCGCCAGCCTGAGCGGCCAGCA 1380
Qy	1381	GCGCCGCCCTGCCCCGCCGCCGCCCTGCCGCCAGCCACCCAGCGCTACGCCAGCC 1440
Db	1381	GCGCCGCCCTGCCCCGCCGCCGCCCTGCCGCCAGCCACCCAGCGCTACGCCAGCC 1440
Qy	1441	TGCGGCCGCCCTGCCGCCGCCCTGAGCGGCCCTGCCAGCGCTCTCGGCCCTGT 1500

Db	1441	TGCGCAGCCCTCGCCGCCCGCTCACGCAGCCCTCGACCGCTCCCTCGGCTCGACGGACTTCAG 1500
Qy	1501	CCCCACTCTCTTCCCTCCCTCGGGCTCTCGTCTCCGACGACGAGTCGAAGAGC 1560
Db	1501	CCCCACTCTCTTCCCTCCCTCGGGCTCTCGTCTCCGACGACGAGTCGAAGAGC 1560
Qy	1561	ACCTGCTCGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGCGACGCTTCAGTT 1620
Db	1561	ACCTGCTCGACCTGAACCCCAGCTCAAATTGAGAGCATGTCCCTGGCGACGCTTCAGTT 1620
Qy	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTCGAGCCCGCTCCGGCTCGCACT 1680
Db	1621	CGTCGTCGGCGCTCGACCGGGACCTGGATTAACTCGAGCCCGCTCCGGCTCGCACT 1680
Qy	1681	TCGAGTTCCCGGACTACTGCACGCCGGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Db	1681	TCGAGTTCCCGGACTACTGCACGCCGGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Qy	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC 1800
Db	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC 1800
Qy	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA 1860
Db	1801	CGGGGGGGTAGGAGAGGAGAAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA 1860
Qy	1861	GAGTTAAAGAGAAAAGGGAAAAAGAAAGAAAAGTAAGCAGGGCTCGTGCCTGGCT 1920
Db	1861	GAGTTAAAGAGAAAAGGGAAAAAGAAAGAAAAGTAAGCAGGGCTCGTGCCTGGCT 1920
Qy	1921	TCTCGTCGCGATCAAGGAGCGCGCGCGTTGGACCCCGCTCCCATCCCCACCT 1980
Db	1921	TCTCGTCGCGATCAAGGAGCGCGCGCGTTGGACCCCGCTCCCATCCCCACCT 1980
Qy	1981	TCCCGGGCCGGGACCACACTGCCACGCCGGAGGACGCCGGAGGAGAACGGGTAGAC 2040
Db	1981	TCCCGGGCCGGGACCACACTGCCACGCCGGAGGACGCCGGAGGAGAACGGGTAGAC 2040
Qy	2041	AGGGGCACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGGCAC 2100
Db	2041	AGGGGCACCTGTGATTGTTATTGATGTTGATGGCAAAAAAAAAAGGCAC 2100
Qy	2101	TTCGAGTTGCTCCCTTGTGTTGAAGAGACCCCTCCCTCCACGAGCTTCGGAC 2160
Db	2101	TTCGAGTTGCTCCCTTGTGTTGAAGAGACCCCTCCCTCCACGAGCTTCGGAC 2160
Qy	2161	TTGTCGACCCCCAGAACAGGGCAGTTAGTTTCTAGAGACTGAAGGAGTCCTCC 2220
Db	2161	TTGTCGACCCCCAGAACAGGGCAGTTAGTTTCTAGAGACTGAAGGAGTCCTCC 2220
Qy	2221	CTTCTGCATCACCACTGGTTTGTGTTTACCGCTCTGGTCAGAAAGGAGGGAA 2280
Db	2221	CTTCTGCATCACCACTGGTTTGTGTTTACCGCTCTGGTCAGAAAGGAGGGAA 2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAACGGCTCCGG 2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAACGGCTCCGG 2340
Qy	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCAC 2400
Db	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCAC 2400
Qy	2401	GCAGCGAATTCGGCTTGGGGCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 2460
Db	2401	GCAGCGAATTCGGCTTGGGGCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 2460
Qy	2461	AGCCGGAGGAGGAGATGTTGAGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAATG 2520

CC treatment of carcinomas, especially lymphoma carcinomas. In addition, the
 CC present invention describes the use of novel compositions for use in
 CC screening methods. Disclosed is a method for screening for anticancer
 CC activity by detecting a difference between the levels of an expression
 CC product of a cancer associated (CA) gene in a cell in the presence and
 CC absence of an anticancer drug candidate. A difference of at least 50% in
 CC the levels of the expression product in the presence of the anticancer
 CC drug candidate compared to the levels of the expression product in the
 CC absence of the anticancer drug candidate indicates that the anticancer
 CC drug candidate has anticancer activity. The methods and compositions are
 CC useful for screening for anticancer activity and for diagnosing and
 CC treating cancer, specifically breast cancer. Sequences given in AEK60014-
 CC AEK60253 are that of CA nucleic acid sequences including genomic
 CC sequence, mRNA and coding sequence. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 19; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGCTCCAGACTCAGCCGAGAG 60
 |||||||

Db 1 TCCCCCAGATTGAGAAAATCCTCTACTTTAGCACGGCTCCAGACTCAGCCGAGAG 60

Qy 61 ACAGCAAATCTGAGCGCGGTGAGAGAGCAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120
 |||||||

Db 61 ACAGCAAATCTGAGCGCGGTGAGAGAGCAGAGAGAGGGAGAGAGAGACTCTCCAGCTG 120

Qy 121 GGAACATAACTCCTCTGAGAGGCCGAGAACCTCTCCCCAAATCTTTGGGACTTT 180
 |||||||

Db 121 GGAACATAACTCCTCTGAGAGGCCGAGAACCTCTCCCCAAATCTTTGGGACTTT 180

Qy 181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGCCAGTTGGCCCGCGCG 240
 |||||||

Db 181 TCTCTCTTACCCACCTCCGCCCTCGAGGGAGTTGAGGGCCAGTTGGCCCGCGCG 240

Qy 241 CGTCTCTCGGTGCTGGCGTGTCTGGCCCGGGGACCGGGAGGGCCCGCGATCGCGCG 300
 |||||||

Db 241 CGTCTCTCGGTGCTGGCGTGTCTGGCCCGGGGACCGGGAGGGCCCGCGATCGCGCG 300

Qy 301 CGGCCGCCGAGGGTGAGGCCCGTGGCCGCCGCCGAGCCGAGGGCATGGTCAGC 360
 |||||||

Db 301 CGGCCGCCGAGGGTGAGGCCCGTGGCCGCCGCCGAGCCGAGGGCATGGTCAGC 360

Qy 361 AAACCAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGAGAGCTGGACTGGCG 420
 |||||||

Db 361 AAACCAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGAGAGCTGGACTGGCG 420

Qy 421 CGGCCCTCGAGCTGGGATCGCTCCCTCCCCACGCCGGCTCCACGCCCTCACGGCG 480
 |||||||

Db 421 CGGCCCTCGAGCTGGGATCGCTCCCTCCCCACGCCGGCTCACGCCCTCACGGCG 480

Qy 481 GCAAGGCCGACGCCGAGCTGGTGCAGAACCCCCGAGTGGGCACATCAAGGCCATGA 540
 |||||||

Db 481 GCAAGGCCGACGCCGAGCTGGTGCAGAACCCCCGAGTGGGCACATCAAGGCCATGA 540

Qy 541 ACGCTTCATGGTGTGGTCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGGCGACA 600
 |||||||

Db 541 ACGCTTCATGGTGTGGTCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGGCGACA 600

Qy 601 TGCACAACGCCGAGATCTCCAAGCGCTGGCAACGCTGGAAGCTGCTAAAGACAGCG 660

Db	601	TGCACAACGCCGAGATCTCAAGCGCTGGCAAACGCTGAAGCTGCTAAAGACAGCG	660
Qy	661	ACAAGATCCCTTCATTGAGAGGCCAGCAGCCTCGCCTCAAGCACATGGCTGACTACC	720
Db	661	ACAAGATCCCTTCATTGAGAGGCCAGCAGCCTCGCCTCAAGCACATGGCTGACTACC	720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCCAGCTCC	780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCCAGCTCC	780
Qy	781	CGGCCGCCGCTCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG	840
Db	781	CGGCCGCCGCTCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG	840
Qy	841	GCGGCATGGGGCGGGCGGGCGGGAGGAGCAGCAACCGGGGGAGGAGGCGGGGTG	900
Db	841	GCGGCATGGGGCGGGCGGGAGGAGCAGCAACCGGGGGAGGAGGCGGGGTG	900
Qy	901	CGAGTGGCGGCCGCAACTCCAACCGGCCAGAAAAAAGAGCTGCGCTCCAAAGTGG	960
Db	901	CGAGTGGCGGCCGCAACTCCAACCGGCCAGAAAAAAGAGCTGCGCTCCAAAGTGG	960
Qy	961	CGGGCGCGCGGGCTGGGTTAGCAAACCGCACGCCAGCTCATCTGGCAGGGCG	1020
Db	961	CGGGCGCGCGGGCTGGGTTAGCAAACCGCACGCCAGCTCATCTGGCAGGGCG	1020
Qy	1021	GCGGCCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGGG	1080
Db	1021	GCGGCCGCGGGAAAGCAGCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGGG	1080
Qy	1081	CCGCCGCCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA	1140
Db	1081	CCGCCGCCCTGCTGCCCTGGCGCCGCCGACCACACTCGCTGTACAAGGCCGGA	1140
Qy	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCGGCAGCCTCGGCCCGCAGCGCTCGGCC	1200
Db	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCGGCAGCCTCGGCCCGCAGCGCTCGGCC	1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGCTACCTGTCGGGCCCTGGCA	1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCGCTACCTGTCGGGCCCTGGCA	1260
Qy	1261	CGTCGTCGCCGTGGCGCGCTGGCGCGGAGCCGACCCAGCGCACCCCTGGCC	1320
Db	1261	CGTCGTCGCCGTGGCGCGCTGGCGCGGAGCCGACCCAGCGCACCCCTGGCC	1320
Qy	1321	TGTACGAGGAGGAGGGCGGGCTGCTGCCAGCGCCCGACGCCAGCTGAGCGCCAGCA	1380
Db	1321	TGTACGAGGAGGAGGGCGGGCTGCTGCCAGCGCCCGACGCCAGCTGAGCGCCAGCA	1380
Qy	1381	GCGCCGCCCTCGTCCCCGCCGCCGCCCTCGCCCGCCGACCCAGCGCTACGCCAGCC	1440
Db	1381	GCGCCGCCCTCGTCCCCGCCGCCGCCCTCGCCCGCCGACCCAGCGCTACGCCAGCC	1440
Qy	1441	TGCCGCCGCCCTGCCGCCGCCCTCGCAGCGCCCTCGCACCGCTCCCTCGGCCCTGT	1500
Db	1441	TGCCGCCGCCCTGCCGCCGCCCTCGCAGCGCCCTCGCACCGCTCCCTCGGCCCTGT	1500
Qy	1501	CCCACTCTCTCTCTCCCTCGGGCTCTCTCGACGACGAGTTCGAAGACG	1560
Db	1501	CCCACTCTCTCTCCCTCGGGCTCTCTCGACGACGAGTTCGAAGACG	1560
Qy	1561	ACCTGCTCGACCTGAACCCAGCTCAAACATTGAGAGCATGTCCTGGCAGCTCAGTT	1620
Db	1561	ACCTGCTCGACCTGAACCCAGCTCAAACATTGAGAGCATGTCCTGGCAGCTCAGTT	1620

Qy	1621	CGTCGCGCCGCTGACCGGGACCTGGATTAACTCGAGCCCGCTCCGGCTCGCACT	1680
Db	1621	CGTCGCGCCGCTGACCGGGACCTGGATTAACTCGAGCCCGCTCCGGCTCGCACT	1680
Qy	1681	TCGAGTTCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Db	1681	TCGAGTTCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Qy	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC	1800
Db	1741	AGTCAGCATCTCAAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGC	1800
Qy	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA	1860
Db	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGGACAGACGAA	1860
Qy	1861	GAGTTAAAGGAAAGGGAAAAAGAAAAGAAAGTAAAGCAGGGCTCGTTGCCCGCGT	1920
Db	1861	GAGTTAAAGGAAAGGGAAAAAGAAAAGAAAGTAAAGCAGGGCTCGTTGCCCGCGT	1920
Qy	1921	TCTCGCGGATCAAGGAGCGCGCGCTTGGACCCCGCTCCATCCCCACCT	1980
Db	1921	TCTCGCGGATCAAGGAGCGCGCGCTTGGACCCCGCTCCATCCCCACCT	1980
Qy	1981	TCCCAGGGCGGGGACCACACTGCCAGCCGGAGGGACCGGAGGAGGAAGAGGGTAGAC	2040
Db	1981	TCCCAGGGCGGGGACCACACTGCCAGCCGGAGGGACCGGAGGAGGAAGAGGGTAGAC	2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGATGTTGTTGATGCAAAAAAAAAAGCGAC	2100
Db	2041	AGGGCGACCTGTGATTGTTATTGATGTTGTTGATGCAAAAAAAAAAGCGAC	2100
Qy	2101	TTCGAGTTGCTCCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Db	2101	TTCGAGTTGCTCCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC	2160
Qy	2161	TTGTCGACCCCCAGAACAGAGGCGAGTTAGTTCTAGAGACTTGAGAGCTCCCC	2220
Db	2161	TTGTCGACCCCCAGAACAGAGGCGAGTTAGTTCTAGAGACTTGAGAGCTCCCC	2220
Qy	2221	CTTCCTGCATCACCACTTGGTTTATTTGCTTCTGGCAAGAAAGGAGGGAA	2280
Db	2221	CTTCCTGCATCACCACTTGGTTTATTTGCTTCTGGCAAGAAAGGAGGGAA	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAAGGCTCCGG	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTTAAACCGCTGATGAAGACAGAAGGCTCCGG	2340
Qy	2341	GGTGACGAATTGGCGATGGCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Db	2341	GGTGACGAATTGGCGATGGCAGATTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Qy	2401	GCAGCGAATTCCCGTTGGGGCTTTTCTCCCTTTCCCTGGCCCGCTCTGC	2460
Db	2401	GCAGCGAATTCCCGTTGGGGCTTTTCTCCCTTTCCCTGGCCCGCTCTGC	2460
Qy	2461	AGCCGAGGAGGAGATGTTGAGGGAGGAGGCCAGCTGACCGGGCTAGGAAATG	2520
Db	2461	AGCCGAGGAGGAGATGTTGAGGGAGGAGGCCAGCTGACCGGGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCCGTGGAGCGCAGCAGCGGGAGCTAGGGCGGGGGAGGAGGACA	2580
Db	2521	ACCCGAGAACCCCGTGGAGCGCAGCAGCGGGAGCTAGGGCGGGGGAGGAGGACA	2580
Qy	2581	CAGACTGGAAGGGGTTACCGTCAAACCTGAAATGGATTGACGTGGAGCTGGCG	2640
Db	2581	CAGACTGGAAGGGGTTACCGTCAAACCTGAAATGGATTGACGTGGAGCTGGCG	2640

Qy 2641 CGGC GGCTGCTGGGCCTCCGCC TTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2641 CGGC GGCTGCTGGGCCTCCGCC TTTCTACGTGAAATCAGTGAGGTGAGACTTCCC 2700
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 2701 GACCCCGGAGGGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGGCAGTCAGTGGAG 2760
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2701 GACCCCGGAGGGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGGCAGTCAGTGGAG 2760
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 2761 GGC GAGTGGTTTCGGAAAAAAAAAGAAAAAGGG 2797
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2761 GGC GAGTGGTTTCGGAAAAAAAAAGAAAAAGGG 2797

RESULT 10
 AEM95802
 ID AEM95802 standard; cDNA; 2797 BP.
 XX
 AC AEM95802;
 XX
 DT 11-JUN-2007 (revised)
 DT 22-MAR-2007 (first entry)
 XX
 DE Human CML marker gene, SEQ ID NO: 81.
 XX
 KW ss; gene; chronic myelocytic leukemia; genetic marker; diagnostic;
 DNA microarray; gene expression.
 XX
 OS Homo sapiens.
 XX
 PN US2006292623-A1.
 XX
 PD 28-DEC-2006.
 XX
 PF 25-AUG-2006; 2006US-00510798.
 XX
 PR 18-JUN-2001; 2001US-0298914P.
 PR 14-JUN-2002; 2002US-00171581.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 XX
 PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
 XX
 DR WPI; 2007-173869/17.
 DR EMBL; X70683.
 DR PC:NCBI; gi36552.
 DR PC_ENCPRO:NCBI; gi36553.
 XX
 PT Classification of cell sample as chronic phase or blast crisis of chronic
 PT myeloid leukemia involves detecting a difference or similarity in
 PT expression by genes from sample corresponding to a set of specific
 PT markers, relative to control.
 XX
 PS Claim 5; SEQ ID NO 81; 28pp; English.
 XX
 CC The invention relates to classifying a cell sample as chronic phase
 CC chronic myeloid leukemia (CP-CML) or blast crisis chronic myeloid
 CC leukemia (BC-CML) by detecting a difference in the expression by the cell
 CC sample of a first set of several genes relative to a control. The first
 CC set of several genes consist of at least 5 genes corresponding to 366
 CC markers (SEQ ID Nos: 1 - 366, AEM95722-AEM96087). The invention comprises
 CC a kit for determining the progression status of a tissue sample or a
 CC sample of bodily fluid from a human or an animal, comprising at least two
 CC microarrays, each comprising at least 20 of the 366 markers as given in
 CC the specification, and a computer system for determining the similarity
 CC of the level of nucleic acid derived from the markers in a sample to that

CC in the CP-CML template and the BC-CML template. The method involves
 CC computing the aggregate differences in expression of each marker between
 CC the sample and the CP-CML pool or the BC-CML pool, or determining the
 CC correlation of expression, calculated according to the equation as given
 CC in the specification, of the markers in the sample to the expression in
 CC the CP-CML and BC-CML pools. The microarray for distinguishing CP-CML
 CC from BC-CML cell samples comprises a positionally-addressable array of
 CC polynucleotide probes bound to a support, the polynucleotide probes
 CC comprising a sequence complementary and hybridizable to a different gene
 CC corresponding to one of the markers. The method for classifying a sample
 CC as CP-CML or BC-CML involves labeling and detecting nucleic acids derived
 CC from a sample with a first fluorophore to obtain a first pool of
 CC fluorophore-labeled nucleic acids, labeling with a second fluorophore a
 CC first pool of nucleic acids derived from two or more CP-CML samples, and
 CC a second pool of nucleic acids derived from two or more BC-CML samples,
 CC contacting the first fluorophore-labeled nucleic acid and the first pool
 CC of second fluorophore-labeled nucleic acid with the first microarray
 CC under hybridization conditions, and contacting the first fluorophore-
 CC labeled nucleic acid and the second pool of second fluorophore-labeled
 CC nucleic acid with the second microarray under hybridization conditions.
 CC The similarity between the expression of the markers is calculated by
 CC determining a first sum of the differences of expression levels for each
 CC marker between the first fluorophore-labeled nucleic acid and the first
 CC pool of second fluorophore-labeled nucleic acid, and a second sum of the
 CC differences of expression levels for each marker between the first
 CC fluorophore-labeled nucleic acid and the second pool of second
 CC fluorophore-labeled nucleic acid, where if the first sum is greater than
 CC the second sum, the sample is classified as CP-CML, and if the second sum
 CC is greater than the first sum, the sample is classified as BC-CML. The
 CC method provides accurate determination of different phases (chronic phase
 CC or blast crisis) of chronic myeloid leukemia (CML), thereby allowing the
 CC determination of treatment options, prognosis and likelihood of
 CC therapeutic response. The present sequence is that of one of the human
 CC marker genes of the current invention.

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 2797 BP; 547 A; 880 C; 931 G; 439 T; 0 U; 0 Other;

Query Match 100.0%; Score 2797; DB 22; Length 2797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTCCCCAGCATTCGAGAAAACTCCTCTACTTACAGCGCTCCAGACTCAGCCGAGAG 60
Db	1	TTCCCCAGCATTCGAGAAAACTCCTCTACTTACAGCGCTCCAGACTCAGCCGAGAG 60
Qy	61	ACAGCAAACCTGCAGCGGGTGAGAGGCGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120
Db	61	ACAGCAAACCTGCAGCGGGTGAGAGGCGAGAGAGAGGGAGAGAGACTCTCCAGCTG 120
Qy	121	GGAACTATAACTCCTCTCGCAGAGGCCGAGAACTCCTCCCCAAATCTTGGGACTTT 180
Db	121	GGAACTATAACTCCTCTCGCAGAGGCCGAGAACTCCTCCCCAAATCTTGGGACTTT 180
Qy	181	TCTCTCTTACCCACCCTCGGCCCTCGAGGGAGTTGAGGGGGCAGTTCGGCCGCGCG 240
Db	181	TCTCTCTTACCCACCCTCGGCCCTCGAGGGAGTTGAGGGGGCAGTTCGGCCGCGCG 240
Qy	241	CGTCTCCCGTTCGGCGTGTGCTTGGCCCGGGAACCGGGAGGGCCGGATCGCGCGG 300
Db	241	CGTCTCCCGTTCGGCGTGTGCTTGGCCCGGGAACCGGGAGGGCCGGATCGCGCGG 300
Qy	301	CGGCCGCCGCGAGGGTGTGAGCGCGCTGGCGCCGCCGAGCGAGGCCATGGTGCAGC 360
Db	301	CGGCCGCCGCGAGGGTGTGAGCGCGCTGGCGCCGCCGAGCGAGGCCATGGTGCAGC 360

Qy	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGCAGAGCTCGGACTCGGGCG 420
Db	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCCGGCAGAGCTCGGACTCGGGCG 420
Qy	421	CCGGCCTCGAGCTGGGAATGCCCTCCCCACGCCGGCTCCACGCCCTCACGGGGCG 480
Db	421	CCGGCCTCGAGCTGGGAATGCCCTCCCCACGCCGGCTCCACGCCCTCACGGGGCG 480
Qy	481	GCAAGGCCGACGCCGAGCTGGTCAAGACCCCCGAGTGCGGACATCAAGGCCCATGA 540
Db	481	GCAAGGCCGACGCCGAGCTGGTCAAGACCCCCGAGTGCGGACATCAAGGCCCATGA 540
Qy	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGCCGCAAGATCATGGAGCAGTCGGCGACA 600
Db	541	ACGCCCTCATGGTGTGGTCAGATCGAGCGCCGCAAGATCATGGAGCAGTCGGCGACA 600
Qy	601	TGCACAACGCCGAGATCTCCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Db	601	TGCACAACGCCGAGATCTCCAAGCGGCTGGCAAACGCTGGAAGCTGCTCAAAGACAGCG 660
Qy	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCAGCTGGCTGCGCTCAAGCACATGGCTGACTACC 720
Db	661	ACAAGATCCCTTCATTGAGAGGGCGGAGCAGCTGGCTGCGCTCAAGCACATGGCTGACTACC 720
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACCTCAGCTCT 780
Qy	781	CGGCCGCCGCCTCCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCGCCTCCCTCCAAGCGGGGGAGAAGGGAGACAAGGTGGCAGTGGCGGG 840
Qy	841	CGGCCATGGGGCGCCGGCGCCGGCGGGAGCACCAAGCGGGGGAGGAGGCCGGTG 900
Db	841	CGGCCATGGGGCGCCGGCGCCGGAGCACCAAGCGGGGGAGGAGGCCGGTG 900
Qy	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Db	901	CGAGTGGCGCGGCCAACCTCAAACCGCGCAGAAAAGAGCTGCGCTCCAAAGTGG 960
Qy	961	CGGGCGGCCGGCGGGCGGTGGGGTAGCAAACCGCACGCCAACCTCATCTGGCAGGCCG 1020
Db	961	CGGGCGGCCGGCGGTGGGGTAGCAAACCGCACGCCAACCTCATCTGGCAGGCCG 1020
Qy	1021	CGGCCGCCGGAAAGCACGCCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGG 1080
Db	1021	CGGCCGCCGGAAAGCACGCCGCTGCCGCCGCCCTCTGCCGCCAACAGGCCGG 1080
Qy	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCAACACTCGCTGTACAAGGCCGGA 1140
Db	1081	CGGCCGCCTGCTGCCCTGGCGCCGCCGACCAACACTCGCTGTACAAGGCCGGA 1140
Qy	1141	CTCCCAGGCCCTGCCCTCCGCCCTCCGCCAGCCTGCCCTCCGCCAGCCTGCC 1200
Db	1141	CTCCCAGGCCCTGCCCTCCGCCCTCCGCCAGCCTGCCCTCCGCCAGCCTGCC 1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTACCTGTTGGCCGGCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTACCTGTTGGCCGGCTGGCA 1260
Qy	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCCGGAGCCGACCCAGCGACCCCTGGCC 1320
Db	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCCGGAGCCGACCCAGCGACCCCTGGCC 1320
Qy	1321	TGTACGGAGGAGGGAGGCCGCCGGCTGCTGCCGAGCGCCAGCCCTGAGGCCAGCA 1380

Db	1321	TGTACGAGGAGGGCGCGGGCTGCTCGCCGAGCAGCCCAGCTGAGCGCCGAGCA	1380
Qy	1381	GCGCCGCCCTGCTCCCCGCCGCCGCCCTCGCCCGACCACCGCGCTACGCCAGCC	1440
Db	1381	GCGCCGCCCTGCTCCCCGCCGCCGCCCTCGCCCGACCACCGCGCTACGCCAGCC	1440
Qy	1441	TGCGCGCCGCCCTCGCCCGCCGCCGCCCTCGCCCGACCACCGCGCTCGGCCTCGT	1500
Db	1441	TGCGCGCCGCCCTCGCCCGCCGCCGCCCTCGCCCGACCACCGCGCTCGGCCTCGT	1500
Qy	1501	CCCACTCCCTCTCCCTCCCTCGGGCTCTCGTCCCTCCGACGACGAGTCGAAGACG	1560
Db	1501	CCCACTCCCTCTCCCTCCCTCGGGCTCTCGTCCCTCCGACGACGAGTCGAAGACG	1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAACTTGAGAGCATGTCCTGGCAGCTCAGTT	1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAACTTGAGAGCATGTCCTGGCAGCTCAGTT	1620
Qy	1621	CGTCGTCGGCGCTGACCGGGACCTGGATTAACTTCGAGCCGGCTCCGGCTCGCACT	1680
Db	1621	CGTCGTCGGCGCTGACCGGGACCTGGATTAACTTCGAGCCGGCTCCGGCTCGCACT	1680
Qy	1681	TCGAGTTCCCGGACTACTGACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Db	1681	TCGAGTTCCCGGACTACTGACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG	1740
Qy	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAGGGCGCAGGCAGGGAGAAGGGC	1800
Db	1741	AGTCAGCATTCACCTGGTTTCACCTACTGAGGGCGCAGGCAGGGAGAAGGGC	1800
Qy	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGACAGACGAA	1860
Db	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGACAGACGAA	1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAAAGTAAGCAGGGCTCGTTCGCCCGGT	1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAAAGTAAGCAGGGCTCGTTCGCCCGGT	1920
Qy	1921	TCTCGTCGCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT	1980
Db	1921	TCTCGTCGCGGATCAAGGAGCGCGGCCGTTGGACCCCGCTCCCATCCCCACCT	1980
Qy	1981	TCCCGGGCGGGGACCACTCTGCCACGCCGGGAGGGACCGGGAGGAGGAAGAGGGTAGAC	2040
Db	1981	TCCCGGGCGGGGACCACTCTGCCACGCCGGGAGGGACCGGGAGGAGGAAGAGGGTAGAC	2040
Qy	2041	AGGGCGACCTGTGATTGTTATTGTGTTGATGCCAAAAAAAGCGAC	2100
Db	2041	AGGGCGACCTGTGATTGTTATTGTGTTGATGCCAAAAAAAGCGAC	2100
Qy	2101	TTCGAGTTGCTCCCTTGCTGAGAGACCCCTCCCCCTCCAACGAGCTCCGGAC	2160
Db	2101	TTCGAGTTGCTCCCTTGCTGAGAGACCCCTCCCCCTCCAACGAGCTCCGGAC	2160
Qy	2161	TTGTCGACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTGAGAGACTCTCCC	2220
Db	2161	TTGTCGACCCCCAGCAAGAAGGCAGTTAGTTCTAGAGACTGAGAGACTCTCCC	2220
Qy	2221	CTTCCCTGCATCACCACTTGGTTTGTGTTTCTGGTCAGAAAGAGGGGA	2280
Db	2221	CTTCCCTGCATCACCACTTGGTTTGTGTTTCTGGTCAGAAAGAGGGGA	2280
Qy	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGCGTGTGAAGACAGAAGGCTCCGG	2340
Db	2281	GAACCCAGCGCACCCCTCCCCCTTTTAAACCGCGTGTGAAGACAGAAGGCTCCGG	2340
Qy	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC	2400

Db	2341	GGTGACGAATTGGCCGATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCAC	2400
Qy	2401	GCAGCGAATTCCTTGGGCTTTCTCCCTCTTCCCCTGCCCCCTCTGC	2460
Db	2401	GCAGCGAATTCCTTGGGCTTTCTCCCTCTTCCCCTGCCCCCTCTGC	2460
Qy	2461	AGCCGAGGAGGAGATGTTGAGGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Db	2461	AGCCGAGGAGGAGATGTTGAGGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG	2520
Qy	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGAGCTAGGGCGGGCGAGGAGGACA	2580
Db	2521	ACCCGAGAACCCGTTGAAGCGCAGCAGCGGAGCTAGGGCGGGCGAGGAGGACA	2580
Qy	2581	CGAACTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Db	2581	CGAACTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCG	2640
Qy	2641	CGGGGGCTGCTGGGCCTCCGCCTCTTACGTGAAATCAGTGAGGTGAGACTTCCA	2700
Db	2641	CGGGGGCTGCTGGGCCTCCGCCTCTTACGTGAAATCAGTGAGGTGAGACTTCCA	2700
Qy	2701	GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Db	2701	GACCCGGAGCGTGGAGGAGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGGAG	2760
Qy	2761	GGCGAGTGGTTCGGAAAAAAAAAAAAAGAAAAAAAGGG	2797
Db	2761	GGCGAGTGGTTCGGAAAAAAAAAAAAAGAAAAAAAGGG	2797

RESULT 11

ADE95783

ID ADE95783 standard; DNA; 2797 BP.

XX

AC ADE95783;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human DNA related to SOX4 gene mRNA.

XX

KW cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy; lymphoma; breast cancer; prostate cancer; leukaemia; ds; human; SOX4.

XX

OS Homo sapiens.

XX

PN WO2003039484-A2.

XX

PD 15-MAY-2003.

XX

PF 08-NOV-2002; 2002WO-US036071.

XX

PR 08-NOV-2001; 2001US-00052482.

XX

PA (SAGR-) SAGRES DISCOVERY.

XX

PI Morris DW, Engelhard EK;

XX

DR WPI; 2003-441462/41.

XX

PT New carcinoma associated nucleic acids and proteins, useful for screening drug candidates, or for diagnosing and treating carcinomas, e.g.

PT lymphoma, breast cancer, prostate cancer or leukemia.

XX

PS Claim 1; SEQ ID NO 41; 793pp; English.

XX

CC This invention relates to novel recombinant nucleic acids for use in
 CC diagnosis and treatment of cancer, especially carcinomas, as well as the
 CC use of compositions in screening methods. The compositions of the
 CC invention may have cytostatic activity whilst the disclosed sequences may
 CC be useful for gene therapy. The carcinoma associated nucleic acids and
 CC proteins are useful for diagnosing and treating carcinomas, for example
 CC lymphoma, breast cancer, prostate cancer or leukaemia, or for screening
 CC drug candidates or bioactive agents capable of binding to, or modulating
 CC the activity of, a carcinoma associated protein. The present sequence is
 CC a DNA sequence which represents the mRNA derived from the human SOX4 gene
 CC which is a carcinoma associated gene of the invention.
 XX

SQ Sequence 2797 BP; 547 A; 881 C; 930 G; 439 T; 0 U; 0 Other;

Query Match	99.9%	Score 2795.4;	DB 9;	Length 2797;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2796;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	TTCCCCAGCATTGAGAAA	CTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG	60
Db	1	TTCCCCAGCATTGAGAAA	CTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAG	60
Qy	61	ACAGCAAATCGAGCGGCTGAGAGAGCGAGAGAGGGAGAGAGACTCTCAGCTG	120	
Db	61	ACAGCAAATCGAGCGGCTGAGAGAGCGAGAGAGGGAGAGAGAGACTCTCAGCTG	120	
Qy	121	GGAACATAACTCCTCTCGAGAGGCCAGACTCCTCCCCAA	TCTTGGGACTTT	180
Db	121	GGAACATAACTCCTCTCGAGAGGCCAGACTCCTCCCCAA	TCTTGGGACTTT	180
Qy	181	TCTCTTTACCCACCTCCGCCCTCGCAGAGGTGAGGGGCAGTTCGGGCGCGCG	240	
Db	181	TCTCTTTACCCACCTCCGCCCTCGCAGAGGTGAGGGGCAGTTCGGGCGCGCG	240	
Qy	241	CGTCTCCCGTTCGGCGTGTCTGGCCGGGAA	CCGGAGGGCCCGCATCGCGCG	300
Db	241	CGTCTCCCGTTCGGCGTGTCTGGCCGGGAA	CCGGAGGGCCCGCATCGCGCG	300
Qy	301	CGGCCGCCGCGAGGGTGAGCGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTG	CAG	360
Db	301	CGGCCGCCGCGAGGGTGAGCGCGCGTGGCGCCGCCGAGCCGAGGCCATGGTG	CAG	360
Qy	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCGCCGCCGAGCCGAGGCCATGGTG	CAG	420
Db	361	AAACCAACAATGCCGAGAACCGGAAGCGCTGCTGGCGCCGCCGAGCCGAGGCCATGGTG	CAG	420
Qy	421	CCGGCCTCGAGCTGGAA	TGCCCTCTCCCCACGCCCGCTCCACGCCCTCACGGCG	480
Db	421	CCGGCCTCGAGCTGGAA	TGCCCTCTCCCCACGCCCGCTCCACGCCCTCACGGCG	480
Qy	481	GCAAGGCCGACGACCCGAGCTGGTGCAGATCGAGCGGCAGAGCTGGCACATCAAGCGACCCATGA	540	
Db	481	GCAAGGCCGACGACCCGAGCTGGTGCAGATCGAGCGGCAGAGCTGGCACATCAAGCGACCCATGA	540	
Qy	541	ACGCCCTCATGGTGTGGTCGAGATCGAGCGGCAGAGCTGGAGCCAGTGGCACATGGAGCAGTC	GGCCGACA	600
Db	541	ACGCCCTCATGGTGTGGTCGAGATCGAGCGGCAGAGCTGGCACATGGAGCAGTC	GGCCGACA	600
Qy	601	TGCACAACGCCGAGATCTCAAGCGCTGGCAAACGCTGGAGCTGCTCAAAGACAGCG	660	
Db	601	TGCACAACGCCGAGATCTCAAGCGCTGGCAAACGCTGGAGCTGCTCAAAGACAGCG	660	
Qy	661	ACAAGATCCCTTCATTGAGAGGCCAGCGCTGGCTGCGCTCAAGCACATGGCTGACTACC	720	
Db	661	ACAAGATCCCTTCATTGAGAGGCCAGCGCTGGCTGCGCTCAAGCACATGGCTGACTACC	720	
Qy	721	CCGACTACAAGTACCGGCCAGGAAGAGGTGAAGTCGGCAACGCCA	CTCAGCTCT	780

Db	721	CCGACTACAAGTACCGGCCAGGAAGAAGGTGAAGTCGGCAACGCCAACTCCAGTCCT 780
Qy	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGCGGG 840
Db	781	CGGCCGCCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGCGGG 840
Qy	841	GCGGCATGGGGCGGCCGGCGCGCGGGAGCAGCAACGCCGGGGAGGAGGCCGGTG 900
Db	841	GCGGCATGGGGCGGCCGGCGCGGGAGCAGCAACGCCGGGGAGGAGGCCGGTG 900
Qy	901	CGAGTGGCGCGCGCCAACCTCAAACCGCGCAGAAAAGAGCTCGGCCTCAAAGTGG 960
Db	901	CGAGTGGCGCGCGCCAACCTCAAACCGCGCAGAAAAGAGCTCGGCCTCAAAGTGG 960
Qy	961	CGGGCGCGCGGGCGGTGGGGTAGCAAACCGCACGCCAACGCTCATCTGGCAGGCCG 1020
Db	961	CGGGCGCGCGGGCGGTGGGGTAGCAAACCGCACGCCAACGCTCATCTGGCAGGCCG 1020
Qy	1021	CGGGCGCGGGAAAGCACGCCGTGCCGCCGCCCTCTGCCGCCAACAGCGGGGG 1080
Db	1021	CGGGCGCGGGAAAGCACGCCGTGCCGCCGCCCTCTGCCGCCAACAGCGGGGG 1080
Qy	1081	CGGCCGCTCTGCCCCGGCGCCGCCGACCACCACTCGCTGTACAAGGCGCGGA 1140
Db	1081	CGGCCGCTCTGCCCCGGCGCCGCCGACCACCACTCGCTGTACAAGGCGCGGA 1140
Qy	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCGCAGCGCTCGGCCCTCCGAGCGCTCGGCC 1200
Db	1141	CTCCCAGCGCTCGGCCCTCCGCCCTCGCAGCGCTCGGCCCTCCGAGCGCTCGGCC 1200
Qy	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTACCTGTTGGGGCTGGCA 1260
Db	1201	CGGGCAAGCACCTGGCGAGAAGAAGGTGAAGCGCTACCTGTTGGGGCTGGCA 1260
Qy	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCGGGAGCGCACCCAGCGCACCCCTGGGC 1320
Db	1261	CGTCGTCGCGCCGTGGCGCGCTGGCGCGGGAGCGCACCCAGCGCACCCCTGGGC 1320
Qy	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCAGCGGCCAGCGCTGAGCGCCCGACCA 1380
Db	1321	TGTACGAGGAGGAGGGCGCGGGCTGCTGCCAGCGGCCAGCGCTGAGCGCCCGACCA 1380
Qy	1381	CGCCGCCCTCGCCCCGCCGCCGCCCTCGCCGCCGACCACCGCGCTACGCCAGCC 1440
Db	1381	CGCCGCCCTCGCCCCGCCGCCGCCCTCGCCGCCGACCACCGCGCTACGCCAGCC 1440
Qy	1441	TGCGCCGCCCTCGCCGCCGCCCTCGCAGCGGCCCTCGCAGCGCCCTCGAGCGCC 1500
Db	1441	TGCGCCGCCCTCGCCGCCGCCCTCGCAGCGGCCCTCGCAGCGCCCTCGAGCGCC 1500
Qy	1501	CCCACTCTCTCTTCTCCCTCGGGCTCTCGTCTCCGACGACGAGTCGAAGACG 1560
Db	1501	CCCACTCTCTCTTCTCCCTCGGGCTCTCGTCTCCGACGACGAGTCGAAGACG 1560
Qy	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTTCAGTT 1620
Db	1561	ACCTGCTGACCTGAACCCAGCTCAAATTGAGAGCATGTCCTGGCAGCTTCAGTT 1620
Qy	1621	CGTCGCGCCCTCGACCGGACCTGGATTAACTTCGAGCCGGCTCCGACTCGCACT 1680
Db	1621	CGTCGCGCCCTCGACCGGACCTGGATTAACTTCGAGCCGGCTCCGACTCGCACT 1680
Qy	1681	TCGAGTTCCGGACTACTGACGCCAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740
Db	1681	TCGAGTTCCGGACTACTGACGCCAGGTGAGCGAGATGATCTCGGGAGACTGGCTCG 1740

Qy	1741	AGTCAGCATCTAACCTGGTTTACCTACTGAGGGCGCGAGGCAGGGAGAAGGGC 1800
Db	1741	AGTCAGCATCTAACCTGGTTTACCTACTGAGGGCGCGAGGCAGGGAGAAGGGC 1800
Qy	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGCACAGC 1860
Db	1801	CGGGGGGGTAGGAGAGGAAAAAAAGTGAAGAAAAGAACGAAAGCACAGC 1860
Qy	1861	GAGTTAAAGAGAAAAGGAAAAAGAAGAAAAGTAAGCAGGGCTCGTTGCCCGCGT 1920
Db	1861	GAGTTAAAGAGAAAAGGAAAAAGAACGAAAGTAAGCAGGGCTCGTTGCCCGCGT 1920
Qy	1921	TCTCGTCGCGATCAAGGAGCGCGCCGTTGGACCCCGCCTCCATCCCCACCT 1980
Db	1921	TCTCGTCGCGATCAAGGAGCGCGCCGTTGGACCCCGCCTCCATCCCCACCT 1980
Qy	1981	TCCCGGGCGGGGACCACCTCTGCCACGCCAGGGAGGACGCCAGGGAGGAGAGGTAGAC 2040
Db	1981	TCCCGGGCGGGGACCACCTCTGCCACGCCAGGGAGGACGCCAGGGAGGAGAGGTAGAC 2040
Qy	2041	AGGGCGACCTGTATTGTGATGGCAAAAAAAAAAGCGAC 2100
Db	2041	AGGGCGACCTGTATTGTGATGGCAAAAAAAAAAGCGAC 2100
Qy	2101	TTCGAGTTGCTCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC 2160
Db	2101	TTCGAGTTGCTCCCTTGCTTAAGAGACCCCTCCCCCTTCCAACGAGCTCCGGAC 2160
Qy	2161	TTGTCGACCCCCAGAACAGGCCAGTTCTAGAGACTTCTAGAGACTTGAAGGAGTCTCCC 2220
Db	2161	TTGTCGACCCCCAGAACAGGCCAGTTCTAGAGACTTCTAGAGACTTGAAGGAGTCTCCC 2220
Qy	2221	CTTCCTGCATACCACCTGGTTTATTTGCTTGGTCAAGAAAGGGGG 2280
Db	2221	CTTCCTGCATACCACCTGGTTTATTTGCTTGGTCAAGAAAGGGGG 2280
Qy	2281	GAACCCAGCGACCCCTCCCCCTTTTAAACCGCTGATGAAGACAGAACGGCTCCGG 2340
Db	2281	GAACCCAGCGACCCCTCCCCCTTTTAAACCGCTGATGAAGACAGAACGGCTCCGG 2340
Qy	2341	GGTGACGAATTGGCGATGCCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Db	2341	GGTGACGAATTGGCGATGCCAGATGTTGGGGAACGCCGGACTGAGAGACTCCAC 2400
Qy	2401	GCAGCGAATTCCGTTGGGCCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 2460
Db	2401	GCAGCGAATTCCGTTGGGCCTTTTCCCTCCCTTTCCCTGGCCCTCTGC 2460
Qy	2461	AGCCGGAGGAGGAGATGTTGGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG 2520
Db	2461	AGCCGGAGGAGGAGATGTTGGGGAGGAGGCCAGCCAGTGTGACCGCGCTAGGAAATG 2520
Qy	2521	ACCCGAGAACCCCTGGGAAGCGCAGCACGGGAGCTAGGGCGGGGGCGAGGAGGACA 2580
Db	2521	ACCCGAGAACCCCTGGGAAGCGCAGCACGGGAGCTAGGGCGGGGGCGAGGAGGACA 2580
Qy	2581	CGAACCTGGAAAGGGGTTACCGTCAAACCTGAAATGGATTGCACTGGGGAGCTGGCG 2640
Db	2581	CGAACCTGGAAAGGGGTTACCGTCAAACCTGAAATGGATTGCACTGGGGAGCTGGCG 2640
Qy	2641	CGGCGCTGCTGGCCTCCGCCTTACGTGAAATCAGTGAGGTGAGACTTCCCA 2700
Db	2641	CGGCGCTGCTGGCCTCCGCCTTACGTGAAATCAGTGAGGTGAGACTTCCCA 2700
Qy	2701	GACCCGGAGGCGTGGAGGAGGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGAG 2760
Db	2701	GACCCGGAGGCGTGGAGGAGGAGACTGTTGATGTGGTACAGGGCAGTCAGTGAG 2760

Qy 2761 GCGAGTGGTTCCGAAAAAAAAAAAAGAAAAAGGG 2797
 ||||||| ||||| ||||| ||||| |||||
 Db 2761 GCGAGTGGTTCCGAAAAAAAAAAAAGAAAAAGGG 2797

RESULT 12
 ADB75556
 ID ADB75556 standard; cDNA; 3233 BP.
 XX
 AC ADB75556;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Prostate cancer marker cDNA.
 XX
 KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003009814-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-US023913.
 XX
 PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;
 PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
 XX
 DR WPI; 2003-248033/24.
 XX
 PT New nucleic acid molecule, useful for diagnosing or treating prostate
 cancer.
 XX
 PS Claim 1; SEQ ID NO 380; 99pp; English.
 XX
 CC The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3233 BP; 662 A; 979 C; 1043 G; 547 T; 0 U; 2 Other;

Query Match 99.9%; Score 2793; DB 8; Length 3233;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCAGCATTGAGAACTCCTCTACTTTAGCACGGTCCAGACTCAGCCGAGAGACAG 64

Db	441	CCAGCATTCGAGAACTCTCTACTTTAGCACGGTCTCCAGACTCAGCGAGAGACAG 500
Qy	65	CAAAC TGCAG CGCG GTGAGAGAGCGAGAGAGAGAGAGAGACTCTCCAGCCTGGAA 124
Db	501	CAAAC TGCAG CGCG GTGAGAGAGCGAGAGAGAGAGAGAGACTCTCCAGCCTGGAA 560
Qy	125	CTATAACT CCTCT CGCG AGAGCG GAGA C TCTTCCC AATCTTTGGGACTTTCTC 184
Db	561	CTATAACT CCTCT CGCG AGAGCG GAGA C TCTTCCC AATCTTTGGGACTTTCTC 620
Qy	185	TCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGCCAGTCGGCCGCCGCGCGTC 244
Db	621	TCTTTACCCACCTCCGCCCTCGCAGGGAGTTGAGGGGCCAGTCGGCCGCCGCGCGTC 680
Qy	245	TTCCC GTT CGCG GTGCTTGCGCCGGGAACC GGAGGGCCCGCGATCGCGCGGGCGC 304
Db	681	TTCCC GTT CGCG GTGCTTGCGCCGGGAACC GGAGGGCCCGCGATCGCGCGGGCGC 740
Qy	305	CGCGCGAGGGGTGTGAGCGCGCTGGGCCCGCGAGGCCATGGTGCAGCAAC 364
Db	741	CGCGCGAGGGGTGTGAGCGCGCTGGGCCCGCGAGGCCATGGTGCAGCAAC 800
Qy	365	CAACAATCGCGAGAACAGGAAGCGCTCTGGCCGGCGAGAGCTCGGACTCGGCGCGG 424
Db	801	CAACAATCGCGAGAACAGGAAGCGCTCTGGCCGGCGAGAGCTCGGACTCGGCGCGG 860
Qy	425	CCTCGAGCTGGGAATCGCTCTCCCCACGCCGGCTCACCGCTCACGGCGCAA 484
Db	861	CCTCGAGCTGGGAATCGCTCTCCCCACGCCGGCTCACCGCTCACGGCGCAA 920
Qy	485	GGCCGACGACCCGAGCTGGTCAAGACCCCGAGTGGCACATCAAGCGACCCATGAACGC 544
Db	921	GGCCGACGACCCGAGCTGGTCAAGACCCCGAGTGGCACATCAAGCGACCCATGAACGC 980
Qy	545	CTTCATGGTGTGGTGCAGATCGAGCGCGCAAGATCATGGAGCTGCGCATGCA 604
Db	981	CTTCATGGTGTGGTGCAGATCGAGCGCGCAAGATCATGGAGCTGCGCATGCA 1040
Qy	605	CAACCGCGAGATCTCCAAGCGCTGGCAAACCGCTGGAGAGCTGCTCAAAGACAGCGACAA 664
Db	1041	CAACCGCGAGATCTCCAAGCGCTGGCAAACCGCTGGAGAGCTGCTCAAAGACAGCGACAA 1100
Qy	665	GATCCCTTCATTGAGAGCGGAGCGGCTGCGCTCAAGCACATGGTCACTACCCGA 724
Db	1101	GATCCCTTCATTGAGAGCGGAGCGGCTGCGCTCAAGCACATGGTCACTACCCGA 1160
Qy	725	CTACAAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCACGCCAACTCCAGCTCTCGGC 784
Db	1161	CTACAAAGTACCGGCCAGGAAGGTGAAGTCCGGCACGCCAACTCCAGCTCTCGGC 1220
Qy	785	CGCCGCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGGGGCG 844
Db	1221	CGCCGCCTCCCTCAAGCGGGGGAGAAGGGAGACAAGGTGGTGGCAGTGGCGGGGGCG 1280
Qy	845	CCATGGGGCGCGCGCGCGCGGGAGAGCACACGGGGGGAGGAGCGGGCGGTGCGAG 904
Db	1281	CCATGGGGCGCGCGCGCGGGAGAGCACACGGGGGGAGGAGGGAGCGGGCGGTGCGAG 1340
Qy	905	TGGCGGGCGGCCAACCTCAAACCGGCCAGAAAAGAGCTCGGGCTCCAAAGTGGCGG 964
Db	1341	TGGCGGGCGGCCAACCTCAAACCGGCCAGAAAAGAGCTCGGGCTCCAAAGTGGCGG 1400
Qy	965	CGGC CGGGCGGTGGGTTAGCAAACCGCACGCCAAGCTCATCTGGCAGCGCGCGG 1024
Db	1401	CGGC CGGGCGGTGGGTTAGCAAACCCACGCCAAGCTCATCTGGCAGCGCGCGG 1460

Qy	1025	CGGGGGAAAGCAGGGCTGCCGCCGCCCTCCGGCGAACAGGGGGGGCGC	1084
Db	1461	CGGGGGAAAGCAGGGCTGCCGCCGCCCTCCGGCGAACAGGGGGGGCGC	1520
Qy	1085	CGCCCTGCTGCCCTGGCGCCGCCGACCAACTCGCTGTACAAGGCACGACTCC	1144
Db	1521	CGCCCTGCTGCCCTGGCGCCGCCGACCAACTCGCTGTACAAGGCACGACTCC	1580
Qy	1145	CAGGCCCTCGGCCCTCCGCCCTCGCAGCCTCGCAGCGCTCGGGCCCCGGG	1204
Db	1581	CAGGCCCTCGGCCCTCCGCCCTCGCAGCCTCGCAGCGCTCGGGCCCCGGG	1640
Qy	1205	CAAGCACCTGGCGAGAAGAAGGTGAAGCGCTTACCTGTTGGCGGCTGGGACGTC	1264
Db	1641	CAAGCACCTGGCGAGAAGAAGGTGAAGCGCTTACCTGTTGGCGGCTGGGACGTC	1700
Qy	1265	GTCGTCGCCCCGCTGGCGCCGCTGGCGCCGGACCCCAGCGACCCCTGGGCTGTA	1324
Db	1701	GTCGTCGCCCCGCTGGCGCCGCTGGCGCCGGACCCCAGCGACCCCTGGGCTGTA	1760
Qy	1325	CGAGGAGGAGGGCGCGGGCTGCTGCCGACGCCAGCTGAGCGGCCAGCGC	1384
Db	1761	CGAGGAGGAGGGCGCGGGCTGCTGCCGACGCCAGCTGAGCGGCCAGCGC	1820
Qy	1385	CGCCCTGTCCCCCGCCGCCGCCGTCGCCGCCGACCCAGCGCTACGCCAGCCTGCG	1444
Db	1821	CGCCCTGTCCCCCGCCGCCGCCGTCGCCGCCGACCCAGCGCTACGCCAGCCTGCG	1880
Qy	1445	CGGCCCTCGCCGCCCGCTCCAGCGCCCTCGCACCGCTCTCGGCCCTCGTCCA	1504
Db	1881	CGGCCCTCGCCGCCCGCTCCAGCGCCCTCGCACCGCTCTCGGCCCTCGTCCA	1940
Qy	1505	CTCCTCTTCTCTCTCGGGCTCTCGCTCCGACGAGTTGAAGACGACCT	1564
Db	1941	CTCCTCTTCTCTCTCGGGCTCTCGCTCCGACGAGTTGAAGACGACCT	2000
Qy	1565	GCTCGACCTGAAACCCAGCTCAAACCTTTGAGAGCATGTCCTGGCAGCTCAGTTCGTC	1624
Db	2001	GCTCGACCTGAAACCCAGCTCAAACCTTTGAGAGCATGTCCTGGCAGCTCAGTTCGTC	2060
Qy	1625	GTCGGCGCTGACCGGGACCTGGATTTAACCTCGAGCCCGCTCGCTCCGACTTCGA	1684
Db	2061	GTCGGCGCTGACCGGGACCTGGATTTAACCTCGAGCCCGCTCGCTCCGACTTCGA	2120
Qy	1685	GTTCCCGGACTACTGCACCCCCGAGGTGAGCGAGATGATCTCGGAGACTGGCTCGAGTC	1744
Db	2121	GTTCCCGGACTACTGCACCCCCGAGGTGAGCGAGATGATCTCGGAGACTGGCTCGAGTC	2180
Qy	1745	CAGCATCTAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGCCGG	1804
Db	2181	CAGCATCTAACCTGGTTTACCTACTGAAGGGCGCAGGCAGGGAGAAGGGCCGG	2240
Qy	1805	GGGGTAGGAGAGGAGAAAAAAAGTAAAAAGAAGAACGAAAAGGACAGACGAAGAGT	1864
Db	2241	GGGGTAGGAGAGGAGAAAAAAAGTAAAAAGAAGAACGAAAAGGACAGACGAAGAGT	2300
Qy	1865	TTAAAGAGAAAAGGAAAAAAAGAAGAAAAGTAAAGCAGGGCTCGTCCGGCGTTCTC	1924
Db	2301	TTAAAGAGAAAAGGAAAAAAAGAAGAAAAGTAAAGCAGGGCTCGTCCGGCGTTCTC	2360
Qy	1925	GTCGTCGATCAAGGAGCGCGCGCGCTTTGGACCCGCTCCATCCCCACCTTCCC	1984
Db	2361	GTCGTCGATCAAGGAGCGCGCGCGCTTTGGACCCGCTCCATCCCCACCTTCCC	2420
Qy	1985	GGGCGGGGGACCCACTCTGCCAGCGGAGGGACGCGGAGGGAGAAGGGTAGACAGGG	2044
Db	2421	GGGCGGGGGACCCACTCTGCCAGCGGAGGGACGCGGAGGGAGAAGGGTAGACAGGG	2480

Qy	2045	GCGACCTGTGATTGTTATTGATGTTGTTGATGCCAAAAAAAAAGCGACTTCG 2104
Db	2481	GCGACCTGTGATTGTTATTGATGTTGTTGATGCCAAAAAAAAAGCGACTTCG 2540
Qy	2105	AGTTTGCTCCCCTTGCTGAAGAGACCCCTCCCCCTCCAACGAGCTCCGGACTTGT 2164
Db	2541	AGTTTGCTCCCCTTGCTGAAGAGACCCCTCCCCCTCCAACGAGCTCCGGACTTGT 2600
Qy	2165	CTGCACCCCCAGCAAGAAGCGAGTTAGTTTCTAGAGACTTGAAGGAGTCCCCCTC 2224
Db	2601	CTGCACCCCCAGCAAGAAGCGAGTTAGTTTCTAGAGACTTGAAGGAGTCTCCCCCTC 2660
Qy	2225	CTGCATCACCACTGGTTTTTATTGCTCTGGTCAAGAAAGGAGGGAGAAC 2284
Db	2661	CTGCATCACCACTGGTTTTTATTGCTCTGGTCAAGAAAGGAGGGAGAAC 2720
Qy	2285	CCAGCGACCCCTCCCCCTTTTTAACCGGTGATGAAGACAGAACGGCTCCGGGTG 2344
Db	2721	CCAGCGACCCCTCCCCCTTTTTAACCGGTGATGAAGACAGAACGGCTCCGGGTG 2780
Qy	2345	ACGAATTGGCGATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCACGCAG 2404
Db	2781	ACGAATTGGCGATGGCAGATGTTGGGGAAACGCCGGACTGAGAGACTCCACGCAG 2840
Qy	2405	GCGAATTCCCGTTGGGCCTTTTCTCTCTCTGGGGCTAGGAAATGACCC 2464
Db	2841	GCGAATTCCCGTTGGGCCTTTTCTCTCTGGGGCTAGGAAATGACCC 2900
Qy	2465	GGAGGAGGAGATGTTGAGGGAGGAGGGCAGCCAGTGACCGCGCTAGGAAATGACCC 2524
Db	2901	GGAGGAGGAGATGTTGAGGGAGGAGGGCAGCCAGTGACCGCGCTAGGAAATGACCC 2960
Qy	2525	GAGACCCCGTGGAAAGCCGACGCCGGGAGCTAGGGCGGGGGAGGAGCACGAA 2584
Db	2961	GAGACCCCGTGGAAAGCCGACGCCGGGAGCTAGGGCGGGGGAGGAGCACGAA 3020
Qy	2585	CTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCGCGC 2644
Db	3021	CTGGAAGGGGTTCACGGTCAAACGTAAATGGATTGACGTTGGGAGCTGGCGCGC 3080
Qy	2645	GGCTGCTGGGCTCCGCCCTTTCTACGTGAAATCAGTGAGGTGAGACTCCCAGACC 2704
Db	3081	GGCTGCTGGGCTCCGCCCTTTCTACGTGAAATCAGTGAGGTGAGACTCCCAGACC 3140
Qy	2705	CCGGAGGCGTGGAGGAGGGAGACTGTTGATGTTGAGCTGGGAGCTGGCGCG 2764
Db	3141	CCGGAGGCGTGGAGGAGGGAGACTGTTGATGTTGAGCTGGCGCG 3200
Qy	2765	AGTGGTTCGGAAAAAAAAGAAAAAAAGGG 2797 2797
Db	3201	AGTGGTTCGGAAAAAAAAGAAAAAAAGGG 3233 3233

RESULT 13

ABV22264

ID ABV22264 standard; cDNA; 4467 BP.

XX

AC ABV22264;

XX

DT 13-SEP-2002 (first entry)

XX

DE Human prostate expression marker cDNA 22255.

XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.

XX